

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 121196

TO: Manjunath N Rao

Location: rem/3b11/3c70

Art Unit: 1652

Friday, May 14, 2004

Case Serial Number: 10/016725

From: Paul Schulwitz

Location: Biotech-Chem Library

REM-1A65

Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Rao,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (571)272-2527



STIC-Biotech/ChemLib

12/196

From:

Rao, Manjunath N.

Sent:

Wednesday, May 05, 2004 10:22 AM

To:

STIC-Biotech/ChemLib

Subject:

Sequence search request for 10/016,725

From:

Manjunath N. Rao

Art Unit 1652, Room 10A11 Mail Box in Room 10D 01

Phone: 306-5681

Date: 5-5-04

Please search the following as soon as possible for application with serial number 10/016725

- 1. Nucleotides 1-3958 of SEQ ID NO: 15
- 2. Nucleotides 1-3910 of SEQ ID NO:15

against all **commercial nucleic acid databases** including **issued patents database** and **pending application database** and provide **a print of all results**.

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao Art Unit 1652, Room 3B81, Mail Box in Room 3C70, Remsen Building, USPTO 400, Dulany St. Alexandria, VA. Phone: 571-272-0939

Searcher:_____Phone:_____
Location:_____
Date Picked Up:_____
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REFERENCE AUTHORS TITLE JOURNAL

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SUMMARIES

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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
  Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Bia Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 151339 bases at least Q40 consensus quality: 15517 bases at least Q20 Consensus quality: 15517 bases at least Q20 Insert size: 167000; agarose-fp Insert size: 167000; agarose-fp Quality coverage: 4.9 in Q20 bases; sum-of-contigs Quality coverage: 5.2 in Q20 bases; sum-of-contigs
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Homo sapiens clone RP11-2M13, WORKING DRAFT SEQUENCE, 12 unordered
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 159351)

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All repeats were identified using RepeatMasker:
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-2M13
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Homo sapiens (human)
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Qy 2043 GGCAGGAGAATTTCTTGAACCCGGGAGGCAGAGGTGAAGCGAGATCACCACT 2102 Db 57350 GGCAGGAGATTTCTTGAACCCGGGAGGCTTGCAGTGAAGCGAGATCACCACCT 57291 Qy 2103 GCACTCCAGCCTGGGGAGAGCTTCCTCTCAAAAAACAAAAACAAAAGAT 2162 Db 57290 GCACTCCAGCCTGGGGAGAGCGAGACTTCCTCTCAAAAAACAAAAACAAAAAAAA	CTGG CTGG CTGG CTGG CTGG CTGG CTGG CTGG	GGCATGGAAGGACACCGGGTGAATGCTTCATAGGCTGGTTCTGAGGTCTCATGGT GGCATGGAAGGACACCGGGTGAATGCATAGCCTGCCTGGTTCTGAGGTCTCATGGT GGCATGGAAGGACCGGGTGATGCTTGCTTGCTTCTGAGCTCTCATGGT GCTCTACAGACACGGAAAAGATGCGGGGCACAGGGACCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGCTCAGAGCACCTACAGAGCACAGGACAGGGACAGGGACAGGGACAGGGACAGGGACAGGGACAGAGCTCAGAGCTCAGAGCTCAGAGCACAGAGACAGAGCACAGAGCACAGAGCACAGAGCACAGAGCACAGAGCACACAGAGCTCAGAGCTCAGAGCACAGAGACACAGAGACACAGAGACAATAGGTCCTGAGGGATTAAAAGACTTGGGCTCTCATATG	TTCTGGGCTCAACTGCCAGCTCGTCACTTACTGGTTGACCATGGGCAAGTTATT T	2843 TGTGCGGCCGGTGTTCTTATTCCACATCCAGCCCTTTGGCCTGGTGGGTG

QY 363 CATATCATATTATAGAGACAGGTTCTCACTCTGTCACCCAGGCTGCAGTGCAGTGGCAC 422 Db 64952 CATATCATATTAGAGACAGGTTCTCACTCTGTCACCCAGGCTGCAGTGCACTGGCAC QY 423 AATCATAGCTCACTGTAACCTCAAACTCCTGGGCTCAAGTGCTACTACCTCAGCCTC Bb 65012 AATCATAGCTCACTGTAACCTCAAACTCCTGGGCTCAAGTGATCCTACTACCTCAGCCTC QY 483 CAGAGTAGCTAAGGACTACAGGCACACACAGGCTCAAGTGATCTTTTTTTT		723 ATGCCTGGCTGATATTTTTTTTGAAACGGGTATCACTCTGTTGCCCAGGCTGGAGT 7 [00 00 00 00 00 00 00 0	Qy 963 GAGACAAGGTCTCACTAIGTTGCCATGATCCCCCACCTCCCAAAGTGCTCATC 1022	65612 TARTCTGTTCATTAGTCAGTTGACACACTTTAGGTTGTTCCACTTTTGACCATTATG 1083 AATAATACTCCAGTGAATATTCATGTATACATTTGTGGGGCATATGTTTCATTTCGT 65672 AATAATACTCCAGTGAATATTCATGTATACATTTGTGGGCCATATGTTTTCATTTCTGT 65672 AATAATACTCCAGTGAATATTCATGTATACATTTGTGGGGCATATGTTTTCATTTCTGT	Oy 1143 TGGGTTTATATCTAGGAGTGGAATTGCTGGATCCCGGGTAATATTTGACAGGCAGAGTT 1202 1	QY 1263 TITICGGAGTITIAITITIAITATTCIGTTGAAATGGCAGTITGANGAAGATACAGTT 1322 Db 65852 TITICGGAGTITITAITITIAITICGACAAATGTGCAGTITGACAAATGTGACAAGTT 65911 QY 1323 ATACTAAGTGAGAAATTAAGGCTGGAATAAGGCTGCAGTTCAGAGTAAAATCATGAAG 1382	1383 65972 1443
requests: clonerequest@sanger.ac.uk On Sep 19, 2001 this sequence version replaced gi:14586033. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30), an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least	one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at		sequence. The true left end of clone KP11-285F16 is at 56886 in this sequence. The true right end of clone RP11-316M21 is at 2000 in this sequence. FEATURES Location/Qualifiers 1. 115778 /mol type="Homo sapiens" //mol type="genomic DNA"		Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 3904; Conservative 0; Mismatches 2; Indels 3; Gaps 3; a GAATTCATCCATTAAATCATAAATCATTAAATGCTTTTAGTAATATTCACAGGTTGTGCAT 62	63 CCATCACAATCCATTTTAGAACAGTTTTATTACTCCAAAAATAAACCCTGCATTCCTTAG 122	TOTGTCTCTATAATTTGCCAATTCTGGACATTCATATAAATGGAAGCAAACAACA TCTGTCTCTATAAATTTGCCAATTCTGGACATTCATATAAATGGAAGCAAACAACA TCTGTCTCTATAAATTTGCCAATTCTGGACATTTTTTAATGGAAGCAAACAACAACAACAACAACAACAACAACAACAAC	64832 GAGACTTGFGACTGCTTTCACTTAGCATTCTATTTTAAGCTCATATGTTACA 64891 303 GTACTTAGCAGTACTTCATTTTTATTCTCAAATGGTATTCCACTGTGGGGTATCC 362

1513 APPLICATION OF THE PROPERTY OF THE PR		2703 ITCTGGGCTCAACTGCTCGTCACTTACTGGTTGCTCTGACCATGGGCAAGTTATT 2762		67471 TACCTGCCAGCTATTCTTATTCCACATCCAAGCCCTTTCGCTGCTGCTGGTGGTGAAACA 67530 2943 CATGTCAGTGTTTCCTGACGGTTTCCAAAGATTCCAAAATTACAACGTGCCAGTC 3002 67531 CATGTCAGTGTTTCCTGACGGTTTCCAAAGAAGATTCCAAAATTACAACCTGCCAGTC 67590					3302 GGGGACGGGAACACGGAACGACGAATGTTAGTGGTGGGCGCCCCCCGAGGGTTCACCACTG 3361 	3362 TITCCTGAGAAACTICCCCAGIGCCCACCCGTTCTCCGIGIGCCCGAGGGCCGGTC 3421 	0 7	3482 CTCCCAACGCGGGATGCCGGGCAGAGGCCCAGCGGCGGGTAGAAGAAGCTGAGAAGGA 3541 	GARACAGAGGGAGGGGAGGCGAGGAGCTGGCGCCAGAGGGAACAGCAGATTGCGCCGAGGGAACAGCAGAATTGCGCCGAGGGAAACAGGAGGGAG	3602 CCAATGGCAACGCACGACGTGGCACCAAATTCCCTTCGGCCAATGACGAGCCGGAG 3661
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45.5%; Score 1779.2; DB 2; Length 185644;
Best Local Similarity 93.8%; Pred. No. 0;
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g of 10951 bp in length
f 100 bp
g of 2167 bp in length
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contig of 2143 bp in length
gap of 100 bp
contig of 4083 bp in length
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contig of 2490 bp in length
gap of 100 bp
contig of 42128 bp in length
gap of 100 bp
contig of 42128 bp in length
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contig of 2268 bp in length
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 3662 TTTACAGAAGCCTCATTAGCATTTCCCCAGAGGCAGGGGAGGGCAGAGGCCGGGTGGT 3721
                                                                                                                                                                                                                CGCACTITGCCCCTGCTTGGCAGCGGATAAAAGGGGGCTGAGGAAAATACCGGACACGGTC 3901
                                                                                                                                                                                                                                                                                                                                                                                                             AL391723 185644 bp DNA linear HTG 11-SEP-2001
Homo sapiens chromosome 10 clone RP11-38B21, WORKING DRAFT
SEQUENCE, 14 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                             68250 TITACAGAAGCCTCATTAGCATTTCCCCAGAGGCAGGGGGGAGGGCAGAGGCCGGGTGGT
                                                                        3722 GIGGIGICGGIGICGGCAGCAICCCCCGGCCCCIGCIGCGGICGCCGGGGAGCCICGGCCI
                                                                                            CTGTCTCCTCCCCCTCCCCCTTACCTCCACGCGGGACCGGCCCGGGCCAGTCAACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 19, 2000 this sequence version replaced gi:10178830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 17502 bases at least Q40
Consensus quality: 179431 bases at least Q30
Consensus quality: 182156 bases at least Q20
Insert size: 184344; sum-of-contigs
Insert size: 140788; 6.0% error; agarose-fp
Quality coverage: 4.15x in Q20 bases; sum-of-contigs Quality
coverage: 6.51x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59110: contig of 59110 bp in length
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61285: contig of 2075 bp in length
61285: gap of 1100 bp
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AL391723/c
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AUTHORS
TITLE
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KEYWORDS
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COMMENT

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OY 3108 ACCAGCCAGCCTGTGTGGGCCGGAGTCCGGTGCGGTCCGGGTGAGCAGCGCGTGGC 3167 Db 182505 ACCAGCCAGCCTGTTGTTGCGGCGGAGTCCGGTGCGGTG	QY 3287 CTGCCACGCGCCTGGGGGCACGGGAAGATGTTAGTGGTGGGCGCCCCC 3346 Db 182325 CTGCCACGCGCT-GGGGAACGGAATGTTAGTGGTGGGCCCCCC 182267 QY 3347 GAGGTTCACCACTGTTTCTGAGAAACTTCCCCAGTGCCCACCCA			181846	RESULT 6 AX431388 LOCUS DEFINITION Sequence 21 from Patent W00240666. ACESSION AX431388 LOCUS ACESSION AX431388. 1 G1:21656235 KEYWORDS SOURCE ORGANISM Homo sapiens (human) ORGANISM Homo sapiens Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. TITLE AUTHORS Enkins, D. K., Winther, M.D., Haardt, M., Goldberg, Y.P., Nwaka, S.O., Ponton, A., Allen, S.J., de Antueno, R.J. and Knickle, L.C. TITLE Fat regulated genes, uses thereof, and compounds for modulating
183544 GGCTCTGACACATAACCAGANNANNANNANNANNANNANNANNANNANNANNANNAN	2208 ACCTACACATTCTGTGCCACATGCCAAGTACTTCTGAGGCATGACTGGATGGCTGTCC 183404 ACGTACAGATTTCTGTGCCACATGCCAAGTACTTCTGAGGCATGACTGGATGAGCTGTCC 2268 ACATCTGAAATCTCTGCCACATGCCAAGTTCTCACGGACAGGACGACGGACG		2627 2627 18298 2687 18292	182925 GCTCTCATATGGTGTTTCTGGGCTCAACTGCTCACTTGTTGCTGTGCTGTGGCTGTGGC 2747 182925 GCTCTCATATGGTGTTTCTGGGCTCAACTGCTCCATCACTTACTGGTTGCTGTGGC 182866 2748 CATGGGCAAGTTATTCCATCTCCATATCTCTTTCCTCACTTTTAAAATGGAATAATGG 2807 182865 CATGGGCAAGTTATTCCATCTCGACATATCTTTTCTCACATTTAAAATGGAATAATGG 182806 2808 GGTACCCACCTCCCAGGGTCACAGAGGGCTTACAGAAAAAGGATTCTTGTGAATTGGCTT 2867 182805 GGTACCCACCTCCCAGGGTCACAGAGAGGCTTACAGAAAAAGGATTCTTGTGAATTGGCTT 2867 182805 GGTACCCACCTCCCAGGGTCACAGAGAGGCTTACAGAAAAGGATTCTTGTGAATTGGCTT 182746	2868 GCAGTAATAATTCAATACCTGCCAGCTATTCTTATTCCACATCCAAGCCCTTTCGCCTGC 2927 182745 GCAGTAATAATTCAATACCTGCCAGCTATTCTTATTCCACATCCAAGCCCTTTCGCCTGC 2927 182745 GCAGTAATAATTCAATACCTGCCAGCTATTCTTATTCCACAAGCCCTTTCGCCTGC 182686 2928 TGCTGGGTGAAAACACATGTCAGTGTTTCCTGACGGTTTCCACAAGAAGAAGTTCCAAAAT 182626 2988 TACAACCTGCCAGTCTGAAGATTTCCTGACGCATCCTGGAGGGGGGGG
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    1970
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Qy 3	3260 AGAICCIGGGGTGCCACGTCTCCCTGCCACGCGCCTGGGGGGACGGGAAGACGGGAAAAA1110 AGAICCTGGGGGGACGGAAGACGGGAAAA1110 AGAICCTGGGGGGGACGGCCACGTCCCCTGCCACGCCCCGGGGGGAC-GGAAGACGGGA	3319
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Qy 3.	3740 GCATCCCGGCGCCCTGCTGCGGTCGCCGAGCCTCGGCCTCTGTCTCCTCCCCCCCC	3799
Qy 31	3800 GCCCTTACCTCCACGGGGACGGCCGGGCCAGTCAACTCCTCGCACTTTGCCCCTGGTTT	3859
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results can be
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Avid (http://baboon.math.berkeley.edu/mavid),
Lagan (http://lagan.stanford.edu/) and paired end information.
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Cercopithecinae; Papio.
1 (bases I to 161827)
Cheng, D. F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R., Peng, Z., Malinov, I. and Rubin, E.M.
Direct Submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was accomplished
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                                                                                                                Unpublished
2 (bases 1 to 161827)
Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R. Peng,Z., Malinov,I. and Rubin,E.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: Plasmid, pUC18
Chemistry: Dye-terminator Big Dye
Assembly program: Phrap veraion 0.990329.

* NOTE: This is a 'working draft' sequence. It currently
* consists of I contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=SCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Funding agent: Programs for Genomic Applications (NHLBI)
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Location/Qualifiers
1. .161827
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Pred. No. 0;
0; Mismatches 134; Indels
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y Vista (http://www-gsd.lbl.gov/VISTA). The
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/mol_type="genomic DNA"
/db_xref="taxon:9557"
/clone="RP41-194B17"
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                                                                                                                                                                                                                                                                                                    Sequence Produced by Berkeley PGA
Web site: http://pga.lbl.gov
Center Code: PGABERK
Center Project Name: B051
Bac Clone Name: RP41-194B17
                                                                                                                                                                                                               Direct Submission
Submitted (08-FEB-2003)
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ilarity 92.3%;
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Best Local Similarity
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	CLIOUNDAONE 3P GENOMIC Sequence AL Unpublished CE 2 (bases 1 to 179879) RS Li,W., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B.,	Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y., Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y., Li,G., Li,C., Bao,Q., Bao,U., Wang,X., Song,L., Zhang,L., Guo,D., Huang,F., Zhang,G., Li,J., Blan,X., Zhang,M., Li,L., Feng,X., Yu,J.) Human Genomic Center, Institute of emy of Sciences, Datun Road, Beijing, Re	100101, P.R.China On May 29, 2000 this sequence version replaced gi:7417472Genome Center Center:Belijna Center	Center code:Beijing Website:http://hgc.igtp.ac.cn http://www.genomics.org.cn Contact.hgc@idtp.ac.cn	Center project Information Center project name:1% project Center clone name: 18, project Center clone name: 8111-799119	Sequencing vector: pUC18; 100% of reads Chemistry: Dye-terminator: ET 55% of reads Chemistry: Dye-terminator Big Dye; 45% of reads	Consensus quality: 149369 bases at least Q40 Consensus quality: 160276 bases at least Q40 Consensus quality: 16726 bases at least Q20 The consensus quality: 16726 bases at least Q20	3 3 1	* NOTE: This is a 'working draft' sequence. It currently consists of all contigs. The true order of the pieces	* arbitrary, days between the contigs sequence record is * arbitrary, days between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence	* as soon as it is available and the accession number will * be preserved. 1 1496: contiq of 1496 bp in length	1596: gap of unknown 2949: contig of 1353	4409: contig of 1360 by in 4509: gap of uknown length	# \$4510 # \$4510 # \$6238
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140606 GGCAGAGCCATTGTTCCCAGGCTGACTGAGCCCCCCAGCGCTCGCCCGGGAGGGA	3238 GCTTCCCGCGTCCCC-AAGCTCCAGATCCTGGGGTGCCTGCCACGTCTCCCTGCCACGG 3296 [3297 CCTGGGGGGACGGAAGACGGGACGAGGATGTTAGTGGTGGGGCCCCCCCGAGGGTTCAC 3356	3357 CACTGITICCIGAGAAACTICCCCAGTGCCCACCCGCTICTCCGTGTGCCCGAGGGC 3416	3417 CGGTCCTGGGCTCGGGGCCCCAAACCGGGTCCCCAGCCCCTTCCAGAGA 3476	3477 GAAAGCTCCCGACGCGGGATGCCGGGCAGAGGCCCAGCGGGGGGGG	3537 AAGGAGAACAGAGGGGAGGGGAGCGAGCTGGCGGCAGAGGAACAGCAGATTGCG 3596 	3597 CCGAGCCAATGGCAACGGCAGGACGAGCACCAAATTCCCTTCGGCCAATGACGAGC 3656 	90000	3776		3777 GGCCTCTGTCTCCCCCTCCCGCCCTTACCTCCACGCGGACCGCGCCCAGTCAA 3836		1*1205 CICCGCGCACIIIGCCCCIGCIIGGGAGGGGAGGGGAGG		ACCESSION ACCESSAS ACCESS
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	misc_reature 9	misc_feature 10	misc_feature 1:	/I misc_feature 14	misc_feature 17		/r misc_feature 20	/r misc_feature 22		misc_feature 27	misc_feature 30	/n misc_feature 33	misc feature 37	/n misc_feature 41	misc_feature 43	misc_feature 46	misc_feature 49	7.11	Query Match Best Local Similarity Matches 1456; Conser	Qy 3 GAATTCATC		Qy 63 CCATCACAA1		Qy 123 CCATCACCC	110075	QY 183 TCTGTCTGT	110135	243	1	LD 110195 GAGACTITGT	Oy 303 GTACTTAGCA	Db 110255 GTACTTAGCA	Oy 363 CATATCATAT	Db 110315 CATATCATAT	OY 423 AATCATAGCT	Db 110375 AATCATAGCT	QY 483 CAGAGTAGCTI
30189: contig	30289: gap of unknown length 33658: contig of 1369 hr in	33758: gap of unknown	37012: Contig of 3154	41069: contig of 4057 41169: gap of unknown	43658: contig of 2489 43758: gap of unknown	contig of 2816 gap of unknown	49890: contig of 321 49990: gap of unknow	53751: Contig of 376 53851: gap of unknow	contig of 352 gap of unknow	61598: contig of 412 61698: gap of unknow	65686: contig of 3988 65786: gap of unknow	70673: contig of 4887 70773: gap of unknown	* 70774 76442: contig of 5669 bp in length * 76443 76542: gap of unknown length	80193: contig of 3651 80293: gap of unknowr	83630: contig of 3337 83730: gap of unknown	89196: contig of 5466 89296: gap of unknown	93491: contig 93591: gap of	99952: contig of 6361 100052: gap of unknown	유혈생	113852: COMCIG OF 8415 113852: gap of unknown 119355: Contig of 5503	119455: gap of unknown 127315: contid of 7860	127415: gap of unknown 137358: contid of 9943	137458: gap of 148311: contid	148411: gap of	160162:	ation/Qualifiers		/ MOJ LYPE="genomic DNA" / Ab Zare="texon:9606" / http://www.news.news.news.news.news.news.news.n	/ CLIT OMOBOME="3" / map="3p"	/clone="RP11-799L19" misc feature 1 1496	feature	misc feature 3050. 4409				wisc feature 7205 alderright"	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGACTGGCTGCTTTCACTTAGCATTCTATTTTAAGGCTCATTATGTTACA 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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Y 99.1%; Pred. No. 0;

:rvative 0; Mismatches 13; Indels 0; G
9114. .10444
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10545. .1213
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12254. .14386
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2478. .27656. .30189
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/ note="assembly_name:Contig28"
/ note="assembly_name:Contig29"
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KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT. SOURCE Lemur catta (ring-tailed lemur)	Σ	_	2 [bases I to 190784) Cheng,JF., Hamilton,M., Peng,Y., Mukhe Peng,Z., Malinov,I. and Rubin,B.M. Direct Submission	AL	Web site: http://pga.lbl.gov Center Code: PGABERR Center Project Name: Lilo Bac Clone Name: LiB2-62P23	This sequence has been compared to sequences of other species using Vista (http://www-gsd.lbl.gov/VISTA). The results can be viewed at	http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=SCD The order-orientation of the draft sequence was accomplished by	using: Avid (http://baboon.math.berkeley.edu/mavid), Lagan (http://lagan.stanford.edu/) and paired end information.	Funding agent: Programs for Genomic Applications (NHLBI) If the Bac Library Name is LBI to LB4, please see website	These libraries are available through the BACPAC Resources Center: http://www.chori.org/bacpac/libraryres.htm as LBNL-1 to LBNL-4.	Summary Statistics: Sequencing vector: Plasmid; pUC18	Chemistry: Dye-terminator big Dye Assembly program: Phrap version 0.990329. * NOTE: This is a "working draft' sequence. It currently * This is a "working draft' sequence. It currently * This is a "working mp, this order of the places."	* consists of a contrage, the true of the sequence record is * is not known and their order in this sequence record is * arbitrary, days between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.	* This record will be updated with the inlished sequence * as soon as it is available and the accession number will * be preserved.	*	source 1190784 /organism="Lemur catta" /mol_type="genomic DNA" /db xref="taxon:9447"	/clone="LB2-62P23" ORIGIN	Query Match Query Match Best Local Similarity 73.3%; Pred. No. 56-179; Matches 1344: Conservative O. Mismatches 134; Indels 106; Gaps 23;	CCTCTCAAAAAACAAAAACAAAAGAATTAAGCAAATTAGACA	Db 120071 AGCCAAAAGAACAAAAAAAAAGAAAAAAAAAAAAAAAA
110435 CAGAGTAGCTAGGACTACAGGCACACACCATACCTGGCTAATTTTTTTT	543 TCATTITATGIATICATITICITICTITITATIGITGITGITGITTIGAGAIAGGGTCTCAC 602 	603 TITGITACCCAGGCTGGAGGCAGTGGCATGGTGACAGCTGAGCGTGACCTTGACTTCCTGG 662 	663 GCTCAAGTGATCCTCCTGCCTCCCCAAGTAGCTGGGACTACAAACACGTGTCACC 722 	723 ANGCCTGGCTGANATTTTTTTTTTTGAAACAGGGTATCACTCTGTTGCCCAGGCTGGAGT 782 	783 ACAGTGGGGTAATAATAGGTCACTGCAGCCTCCCCTGGGGCTCAAGCAATCCGCTGGG 842 	843 CTCAGCATCCTGAGTAGCTGGGACTACAGGCTTGTGCCACCAGGCCCAGCTAAGTTTTAA 902	903 AAAAGATTTTTGGTATAGAGGAGGTCTTGCTATGTTGCTCAGGCTGTATTTTTATTGTT 962 	963 GAGACAAGSTCTCACTATGTTGCCATGATCCCCCCCCCCC	3 TTATCTCTTCATTAGTCAGTGACAGACATTTAGGTTGTTTCCACTTTTGACCATTATG	110975 TTATCTGTTCATTAGTCAGTTGACAGACATTTAGGTTGTTTCCACTTTTGACCATTATG 111034 1083 AATAATACTCCAGTGAATATTCATGTATACATTTGTGTGGGCCATATGTTTTCATTTCTGT 1142		1143 TGGGTTTATATCTAGGAGTGGAATTGCTGGATCCCGGGTAATATTTGACAGGCAGAGTT 1202 	1203 CAGGGGAAGAAAACTTGGGAAAATGAAGCATGTTTAGAAATCAGCAAGAGTTGCGGGGT 1262 	3 ITTTCGGAGTITIATATITIATATICTGTTGACAAATGTGCAGTITTGATGAAGATACAAGTT	racaagtī	1323 ATACTAAGTGAGAAGTGAGAATTAAGGCTGGAATAGGCCTTCAGAGTAAAATCATGAAG 1382 	n n		111395 TTTTTTAAAATAACCGTCATAGTCCAGC 111423	
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HTG 08-FEB-2003

AC139669 190784 bp DNA linear F Lemur catta clone LB2-62P23, WORKING DRAFT SEQUENCE. AC139669 AC139669.1 GI:28273352

RESULT 9
AC139669
LOCUS
DEFINITION
ACCESSION
VERSION

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120071 AGCCAAATGGACTAAGACAAAAGGTAAACCTGCAGTTGGTAAAGCAACAGATCTTCCAA 120130
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                                                                                                                                                                   Sciences, Lawrence Berkeley National srkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to LB4, please see website w-gsd.lbi.gov/cheng/BAC.hbi.gov cheng/BAC.hbi.gov chrough the BACPAC Resources Center: braxyres.htm as LBNL-1 to LBNL-4.
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. 5e-179;
tches 383; Indels 106; Gaps
Y., Mukherjee, S., Hosseini, R.,
                                                                                                    Y., Mukherjee,S., Hosseini,R.,
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Db 121240 GTCTGCCTCCGGGGCCTGGGGACGACGAAGGGAAGGAAGG	0y 3520 GTGGAAGAAGCTGAGAAACAGAGGGGAGGGGAGGGGGGGG	3700 GCAGGGGCAGAGGCCGGTGGTGGTCGGTGTCGGCAGCATCCCCGGCGCCCTGTG 3759	751 GACTGCCTGGCCCAĞTCAACTCTGCACTTTGCCCCTTG 878 GCTGACGAAATACCGGACACGGTCACCCGTTGC 3910	ase variant A (SCD) gene, raniata; Vertebrata; Eute	REFERENCE 1 (bases 1 to 17089) AUTHORS Medrano, J.F., Islas-Trejo, A.D. and Johnson, A.M. TITLE Genomic sequence of the bovine stearoyl-CoA desaturase JUNUNIAL Unpublished AUTHORS Medrano, J.F., Islas-Trejo, A.D. and Johnson, A.M. REFERENCE 2 (bases 1 to 17088) AUTHORS Medrano, J.F., Islas-Trejo, A.D. and Johnson, A.M. TITLE Direct Submission JUNNAL Submitted (21-FEB-2003) Animal Science, University of California, Con Shields Avenue, Davis, CA 95616-8521, USA FRATURES 117088 Source /organism="Bos taurus" //db_xref="taxon:9913" //db_xref="taxon:9913" //db_xref="taxon:9913" //db_xref="taxon:9913" //db_xref="taxon:9913"
Qy 2244 GAGGCATGACTGGATGACTGTCCACATCTGAAATCATCGTTTCAGAACTTTCA 2303 Db 120191 GAGTCATTTCTAGATGAGTGTCCATAGTTGAAACTTTCA 120250 Qy 2304 GACGGACAGGCAGCACGACTGGAATGAGTCCCATTCGGCCCAGAGGTTGGCC 2363 Db 120251 CACTGGACAGGACAGGAATAGAGACTCTCGGTCCAGGCAGAGTTGTC 120310 Qy 2364 TTGACCCTGAGAAGAGGGGAATAGAGACTCTCGGTCCCAGGAATTCC 120310 Qy 2364 TTGACCCTGAGAACAGGAATAGAGCTGCTTAGTCTACCTCCCCAGGAATCCC 120310 Qy 2423 AGGTGCTTGTCTCCTGGGCCAACAAGGGAGCTGCTTAGTCCCTCTCTCT	2483 CCAGGGGAAGGATCTAGGGAAGAAGACTATGGGAAAGACTAGGGCATGGAAGGACACCGGGT 2542	2663 120592 2723 120650	Db 120710 Triccricarctritaalariddaaracrdaacacacricaraagarcracagagarr 120768 Qy 2841 CaGaharcgarrcragaarrcgcracacacacacacacacacaca	OY 2961 CGGTTTCCACAAAGAATTCCAAACTTACAACCTG-CCAGTCTGAAAACTCCCAAAAC 3019 Db 120884 TTTTTCCATTAAGAGTTCCAAAATTACAACCTGACAAATCTGAAAATCTCCAAAAC 120941 OY 3020 ATCCGGCACGCATCCTGGAGGCGGGGTTGGGGATGGGAT	

Jane SCD	/note="compared to sequence in variant B" /replace="g" 1501		<pre>/ replace= u." variation 15202 /gene="SCD" /gene="Compared to sequence in variant B" / root= non-location for the sequence in variant B"</pre>	variation 15284 /gene="SCD" /note="SCD" /note="CD"		variation	/note="compared to sequence in variant B" /replace="t" ORIGIN	Ouery Match 12.8%; Score 500; DB 4; Length 17088; Best Local Similarity 64.6%; Pred. No. 3.8e-111; Matches 1208; Conservative 0; Mismatches 485; Indels 177; Gaps 24,	Qy 2164 AAGCAAATTAGACATTGCAGAGAACCTGAAGGGGGTCAGACCGCGTACAGATTTCTGT 2223	Qy 2224 GCCACATGCCAAGTACTTCTGAGGCATGACTGGATGAGCTGTCCACATCTGAAATC 227	Qy 2280 ATCCAGTCTTGTTCAGAACTTTCACACCGGACAGGAGCCAGGACTGGAATGCAGTCTCC 233	QY 2340 INGTEACTGGCCAGAGAGTIGGCCTTGACCCTGAGACCAACAAGAGGGCTGCT 2399	Qy 2400 IAGICIACCICCCAGGAAAICCCAGGIGCTIGICITCCTGGGAAGIGAAICAIIGGGGCA 2459	Qy 2460 GCACTCCGTATTTCTCCTCTTCCCAGGGAAGGATCCTAGGGCAGTATTTGGGAAAGAC 2519	QY 2520 ATGGGCATGGAAGGACACCGGGTGAATGCATAGCCTGCCT	Qy 2576 GGTAAGGTCCTACAGGAAAAGATGGGGGCACAGGGACAGATCAGTAGGGTCAGA 263 	OY 2636 GCATCTCAGGGCCAATATGGTCCTGAGCAGGATTAAGAGCTTGGGCTCTCAT 269	Qy 2696 ATGGTGTTTGTGGGCTCAACTGCCAGTCCACTTACTGGTTGCTGTGACCAT-GGGC 2754	Qy 2755 AAGTTATTCCATATCTCTCTCTTTTCTCACTTTTAAAATGGAATAATGGGGTA 2811
	/gene="SCD" 11880 //oresincon"	.2850,67206850,8314851	lesaturase variant A" 2850,67206850,8314851 1218)	/gene=~sc /EC_number="1.14.99.5" /note="delta-9 desaturase" /acfor atart-1	<pre>/cocol_scare_1 /product="stearoyl-CoA desaturase variant A" /protein_id="AA063569.1" /db_xref="GI:39469127"</pre>	/cranslation="MRAHLLOBEISSSYTTTTITAPPSRVLQNGGGKLEKTPLYLBE DIRPEMRDDIYDPTYODKEGFKPKLESYWRNITIMSLLHLGALYGTLIPTCKTYTYY WVLFYYLMGALGITAGAHRLMSHRTYKARLPIRVFLIIGNTMAFQNDVFEWSRDHRAH HYRSETDADPHNSRGSFFSHVGMLLVRKHPAVKEKGSTLNLSDLAABKLVWFQRRYR	SLFFATLERYALGLNVTWLVNS TFPYDYSASEYRWHINFTTFFI	e="SCD" e="compared to sequence in variant B lace="g"	e="SCD" e="compared to sequence in variant B lace="g"	e="SCD" e="compared to sequence in variant lace="g"	to sequence in variant	to sequence in variant	"SCD" ="compared to sequence in variant ace="t"	="SCD" ="compared to sequence in variant ace="t"	to sequence in variant	""SCD" ="compared to sequence in variant ace="a"	="SCD" ="compared to sequence in variant ace="t"	="SCD" ="compared to sequence in variant ace="g"	14662 /gene="SCD" /note="compared to seculated in variant D"

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                                                                        Score 460; DB 9; Length 164201;
Pred. No. 3.3e-101;
0; Mismatches 660; Indels 111; Gaps
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/note="Single clone region. Assembly confirmed by restriction digest data."
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Best Local Similarity 58.9%;
Matches 1107; Conservative (
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                                                                    Brownlie, A.J., Hayden, M.R., Attie, A.D., Ntambi, J.M.,
Gray-Keller, M.P. and Miyazaki, M.
Methods and compositions using stearoyl-coa desaturase to identify
triglyceride reducing therapeutic agents
Patent: WO 0162954-A. 13-0406-2001;
Xenon Genetics Inc. (CA); WISCONSIN ALDMNI RESEARCH FOUNDATION
(US); University of British Columbia (CA)
Location/Qualifiers
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                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryotz.

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Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 200288)

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                                                                                                                                                                                                                                                                                                                                                                                                               3459 CCCAGCCCTTCCAGAGAAAAGCTCCCGAGGATGCCGGGCAGAGGCCCAGCGGCG
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200288 bp DNA linear HTG 27-HOMO sapiens chromosome 3 clone RP11-759D18, WORKING DRAFT SEQUENCE, 36 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                        11.5%; Score 450.4; DB 6; Length 617; ilarity 99.8%; Pred. No. 3e-99; Conservative 0; Mismatches 1; Indels 0
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
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Charco, Chen Barch, Cavasos, S.R., Chacko, J., Chavez, D.,
Chaveland, C.D., CoxC. Coop, M. Marky, M. Caracter, D. C.,
Devlaland, C.D., CoxC. Coop, M. Marky, M. Control, S. Coop, M. Caracter, J. Ding, H. B.
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Samharic, C. Marcia, C. Day, Caracilli, L. Ding Y. Dinh, H. H.
Gablai, N. Faragano, D. Tagaer, H. Dugan-Rocha, S., Durbin, X.J.,
Harris, C. Marcia, K. Harr, M. Havlas, P. Hawas, M. Gilling, H. Harris, Harris, H. Harris, M. Macharis, M. Marine, M. Macharis, M. Martine, F. Marchiny, E. Machiny, M. Morris, S. Gott, G. Shen, H. Shoosh, M. Marin, S. Harris, M. Marris, M. Macharis, M. Marris, M. Macharis, M. Marris, M. Macharis, M. Marris, M. Macharis, M. Macharis, M. Marris, M. Macharis, M
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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gap of unknown lease contig of 10316 by
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contig of unknown lease contig of 11851 by
                                                                                                                            contig of 1266 b

gap of unknown 1

gap of unknown 1

gap of unknown 1

contig of 1665 b

gap of unknown 1

contig of 1665 b

gap of unknown 1

contig of 1282 b

gap of unknown 1

contig of 1284 b

gap of unknown 1

gap of unknown 1

contig of 1624 b

gap of unknown 1

contig of 1627 b
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gap of unknown l
contig of 1649 b
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contig of 1154 b
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                                                                                                                                                                                                        2; Length 200288;
10 159469: gap of unknown length

173326: contig of 13857 bp in length

17 173426: gap of unknown length

17 200288: contig of 26862 bp in length.

Location/Qualifiers
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                    Score 447.2; DB 2;
Pred. No. 4.6e-98;
); Mismatches 668;
                                                                           1. .200288
/organism="Homo sapiens"
/orl_type="genomic DNA"
/db_xref="texon:9606"
/chromosome="3"
/clone="RP11-759D18"
                                                                                                                                                                                                                                    ;
0
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 159370
159470
173327
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                                                                                                                                                                                                                        GCTACTCTTTTGCTGAGGCAGGAGAATCGCTTGAACCCCATGAGGCTTAGGTTGTGGTG
                                                                                                                                                                                                                                                                   GCTACTTGGGAGGGTGAGGAAGAGAATTTCTTGAA-CCCGGGAGGCAGAGGTTGCAGTG 2084
                                                                                                                                                                                                                                                                                                                     CCGTCTACTAAAAATACTA--AATTAGCCAGGTGTGGTGGCGCATGCCTGTAATCCCA
                                                                                                                                                                                                                                                                                                                                                             CCGTCTCTACTAAAAATACAAAAAATTAGCTAAGTGTGGTGGCGCATGCCTGTAATCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                          AGGTGAĞCCĞATCACCTGAĞĞTTĞĞĞAĞTTCAAĞACCAACCTĞACCAACGTĞĞAĞAAACC
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                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with mall sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given swissering with their source databases: Em. EMBL; Sw: Swissprof; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP http://www.sanger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RP11-565H13 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-SEP-2002) Wellcome Trust Sanger Institute, Hinxtor Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Sep 30, 2002 this sequence version replaced gi:21694438. Draft Sequence Produced by Genome Therapeutics Corp, 100 Beaver Street, Waltham, MA 02453, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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TTTTTTTTTTTGAGACAGATTCTTGCTCTGTCACCCAGGCTGGACTCCGGCAGAGGCA
                                            TATCATATTATTAGAGACAGGTTCTCACTCTGTCACCCAGGCTGGAGT---GCAGTGGCA 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 175842)
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ALT/31547 AC073586
ALT/31547.9 GI:23380932
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                                                                                                                                                                                                                                   'clone_lib="RPCI-11.2"
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DM clone RP11-565H13 on chromosome
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422 CAATCATAGCTCACTGTAACCTCAAACTCCTGGGCTCAAGTGATCCTACTACCTCAGCCT 481

Db 147780 CTCAGGCTGGAGTGCAATCTCAGTTCACTGCAACCTCTGCCTCCCAGGTTCA 147839 1539 AGCAATTCTCCTGCTTCCAGGTTCA 147839	QY 1659 AAACTITTGCTGTCATAATTGTTGTAACTATTGTTCCTTTTGCTGAGGTAGGGCC 1714 Db 147960 AAACTICTAACCTCAGGCGATCCACCTCAGCTCCCAAAATGCTACAATTATAGGC 148019 QY 1715 CCCAGACCAAAAAAAAATAAATTATAATGATTCAATTGATTG	Db 148080 CTCTTCTATCTGCTTTGAAATATACTACACATTCTTGCTGGCTATAGTCGGCTCACT 148139	QY 1950 CCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAAATTAGCTAAGTGTGGTGGC 2009 Db 148260 CCAACATGGAGAAAACCCCGTCTTACTAAAAATACAAAAACATTAGCCAGCATGGTAGCA 148319 QY 2010 CATGCCTGTAATCCCAGCTACTTGGGAGGGTGAGGCAGAGAATTTCTTGAACCCGGGAG 2069 Db 148320 CATGCCTGTAATCTCAGCTACTTAGGAGGCTGAGGCAGCAAATCGCTTGAACCCGGGAG 148379	QY 2070 GCAGAGGTTGCAGTGAATCACACCACTGCACTGCACTGGGGGGA-GAGAGGGA 2128 Db 148380 GCAGAGGTTGCAGTGAGCCAAGATCGCGCCATTGCACTCCAGCCTGGGCAACAAGAGTGA 148439 QY 2129 GACTTCCTCTCAAAAAAACAAAAAAAAAAAAAAAAAAAA	190508 bp DNA linear 18 BAC clone RP11-469M7 from 2, complete (GI:4827310 18 (human)	REFERENCE I (Dases 1 to 190508) AUTHORS Sulston, "B. and Waterston, R. AUTHORS Sulston, "B. and Waterston, R. TITLE TOWARD a complete human genome sequence GENOMEA GENOME Res. 8 (11), 1097-1108 (1998) PUBMED 9963792 REFERENCE 2 (Dases 1 to 190508) AUTHORS Abbott, A. and Le, T. TITLE TITLE The sequence of Homo sapiens BAC clone RP11-469M7 AUTHORS Abbott, A. and Le, T. TITLE TOWNINAL Unpublished 1 to 190508) REFERENCE 3 (Dases 1 to 190508) AUTHORS Waterston, R.H. TITLE Direct Submission JOURNAL Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
	602 CTTTGTTACCCAGGCTGGAGGCAGTGGCATGGTGAGCTGAGCAGCCTTGACTTCC	Db 147031	F-E 2 F	CC 1065 CC 1065 TG 14735 CA 1125 CT 14741	1126 TATGITTTCATTTCTGTTGGGGTT-TATATCTAGGGGGGGGGGGG	147540 CAGARCTIGGCTIAAACTCICCATTCTCTGTCTATATATATATATATATATATATACCCC 147599 1305 TTGATGAAGATACAAGTTATACTAAAGGGGGATTTAGGGGGGTTTTAGGGGGGTTTTAGGGGGG

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                                                                    Submitted (14-MAY-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, 65 (bases 1 to 190508)
                                                                                                                                                                Direct Submission
Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On May 14, 1999 this sequence version replaced gi:3309089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 511-8. The clone may be obtained either from and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)

VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as Compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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Center washington University Genome Sequencing Center
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MO 63108, USA
4 (bases 1 to 190508)
Waterston, R.H.
Direct Submission
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Best Local Similarity 60.13
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Abl57445 Human ste Abk94819 Human ste Aak26627 Human imm Abg88036 Human imm Abg88096 Human ost Aak60044 Human imm Aas42015 Genomic s Aax90847 Human PAC Aad14749 Human PAC Aad14749 Human rep Ab108012 Human rep Ab108014 Human rep Ab108013 Human rep Ab108014 Human rep Ab4108013 Human rep Ab4108013 Human rep Ab4108013 Human rep Ab4108013 Human rep Ab4108013 Human rep Ab4108013 Human rep Ab4108013 Human rep Ab4108013 Human rep Ab4108013 Human rep Ab4108013 Human rep Ab4108013 Human rep Ab4108013 Human rep Ab41091 Human rep Ab41091 Human rep Ab41091 Human rep Ab41091 Human rep Ab41091 Human rep	
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DNA encod Human cDN	Huma	MP P1	Humar	Humar	Humar	Human GPC	DNA e	Human mus Himan mis	CDNA PACC	ANG	Human GPC	Mouse	Humar	Human	Human	Human :	Cancer ba MRP1 base															=		;												

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/*tag= j /*tag= j //bound_molety= "SREBP" protein_bind 991594 /*tag= v //tag= v	I /bound_moiety= "SREBP" I protein_bind complement(10371040) I /*tag= 1	I /bound_moiety= "AP-1" Protein_bind complement(10731076)		/bound_molety= "C/EBP-beta" protein_bind la141413 **tag="color: blue;"	/bound_moiety= "NF-1" protein_bind complement(14231426)	/bound molety= "HNF3-beta" protein_bind complement(15001503)	/ _cay= q / _cay= d / bound molety= "SREBP" protein_bind complement(1587, .1590)	/bound moiety= "NF-kB" protein_bind l628. 1631	/ ray= b // ray= b // bound_moiety= "NF-kB" // pound_moiety= "NF-kB" // pind complement(1632, .1634) /****	/bound_moiety= "IRF-1" protein_bind 1713. 1716	₽,9	/*tag= v /*tag= v /*tag= v /*tag= v /bound_moiety= "HNF3-beta" protein_bind i8331836	/*tag= w //tag= w //bound moiety= "IRF-2" protein_bind complement(18631866)	protein_bind 1977. 1920	/ rag= y / rag= y /bound moiety= "SREBP" protein_bind 1928 /#f== // ff== / ff==	protein_bind complement(20872090)	E IN	/bound_moiety= "SREBP" protein_bind complement(2116, .2119) /tag= ac	/bound_molety= "AP-2" protein_bind complement(21792182) /*tag= ad	/bound_moiety= "CHOP" protein_bind 2199. 2202 /*tag= a== /*tag= a==	/bound_molety= "RAR-alphal" protein_bind complement(2231. 2234)	/ cas at // hound moiety= "NF-1" protein_bind 22452248	/*tag= ag /*tag= ag /*tag= ag /bound_moiety= "Pax-6" protein_bind 23412344	

841 GCCTCAGCATCCTGAGTAGCTGGGACTACAGGCTTGTGCCACCAGGCCCAGCTAAGTTTT 900 901 AAAAATGATTTTTGGTATAGAGGACTTTGCTATGTTGCTCAGGCTCTATTTTTATTG 960	TGTICATTAGTCAGTTGACAGACATTTAGGTTGTTTTCACTTTTTGACTTGTTCCACTTTTTTGACATATACATTGTGGGGCATATGTTTTCATAGTTGTGGGCATATGTTTTCATGTTTTTCATGTTTTTCATGTTTTTTTT	12		1261 GITTTTCGGAGTTTTATTTTATTTCGGACAGACAGAGTTTGATGAGAGTACAGG 1320 1321 TTATACTAAGTGAGAAGTGAGAATTAAGGCTGGAATAGGGCGTTCAGAGTAAAATCATGA 1380 1321 TTATACTAAGTGAGAAGTGAGAATTAAGGCTGGAATAGGGCGTTCAGAGTAAAATCATCA 1380	144	1441 ITTTTTTTTTTTTGAGAAAAGACTCTTGCTCTTTCACCCTGGAGGGCAGTGGTG 1500 	156	1561 CCCAAGTAGCTGGGACTACAGGCACTTCCCACCATGCCCAGCTGATTTTTGTATTTTTAG 1620 	1621 TAGAGATTTCACTTIGTIGGCCAAGCTGGTCTCAAACTTTTTGCTGTCATAATTG 1680 	1681 TIGTAACTATTGTTCCTTTTGCTGAGGTAGGCCCCCGGACCAAAAAAAA	1741 AATCCAAATCAGTGTTGGTTTGACACTGTCACTTGAGAACCACAGTGTGACCAGGGC 1800 	1801 CTCAGGACTAGAGGTGATCTCTGGTCGAAAGAGAAATAGAAATGAAAATATTCTCCGGGCC 1860 	1861 AGGCGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCATGTGGATCAC 1920 	1921 CTGAGGTCAGGAGTTCAAAACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAA 1980
4 6 4 6 6 6 	ය දුරු සු	8 8 8	6 8 8	g & g	ති ති	B &	B &	QJ QD	<i>≿</i> 41	oy.	<i>8</i>	8 &	oy Op	op ox
FT protein_bind complement (32453248) FT / tag= b / *tag= bh FT protein_bind complement (32763279) FT protein_bind domesty= "Whn" FT protein_bind 32913294 FT protein_bind 32913294 / *tag= bi FT protein_bind 32923295 Query Match Query Match And the following for the following	Matches 3910; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AGGANTCATCCATTAAATCATACATTTAATGGCTTTTAGTATATCACAGGTTGGC 60 Db 1 AGGANTCATCATTAAATCATACATTTAATGGCTTTTAGTATTCACAGGTTGTCC 60	CCTT	121 AGCATCACCCCAACATCTCCTCCTTCCAACCCCTGGGCAACCACCAATCTAC 180 121 AGCCATCACCCCAACATCTCCTCTTTTTTTTTTTTTTTT	181 TTTCTGTCTCTATAAATTTGCCAATTCTGGACATTTCATATAATGGAAGCAACAACAT 240 241 GTGAGACTTTGTGACTGGCTGCTTTCACTTAGCATTCTTTAAGGCTCATTAGTTA 300 [3TAT 3	7997 			541 ITTCAITITAIGIAITCAITITCITITITITITITITITITITITITITITAGAITAGGICIC 600 	601 ACTTIGITACCCAGGCTGGAGGGCAGTGGCATGGCAGCTGAGCAGCCTTGACTTCCT 660 	7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 -		781 GTACAGTGGCGTAATAGCTCACTGCAGCCTCCCCTCCTGGGCTCAAGCAATCCGCTG 840 	TT

Qy 3061 TGCCCGCCCGGTCCTGAACAGGATGCGTGCGCGCAGGCACACACA	, ,,,,,,		QY 3421 CCTGGGCTAGGCTCCCAGCCCCAAACCGGGTCCCCAGCCCCTTCCAGAGAAA 3480 Db 3421 CCTGGGCTAGGCTCCGGCCCCAGCCCCAAACCAGGCCCCATCCAAGAGAAA 3480	3481	3541	3601	QY 3661 GTTTACAGAAGCCTCATTAGCATTTCCCCAGAGGCAGGGGCAGAGGCAGAGGCCGGGTGG 3720 Db 3661 GTTTACAGAAGCCTCATTACCATTTCCCCAGAGGCAGGGGCAGAGGCAGAGGCCAGAGGCAGGGTGG 3720	QY 3721 TGTGGTGTCGGTACCGGCAGCATCCCCGGCGCCTGCTGCGCGCGGGGGCCTCGGCC 3780 Db 3721 TGTGGTGTCGGTGTCGGCAGCATCCCCGGCCCTGCTGCTGCCGCGAGCTCGCCGAGCCTCGGCC 3780	QY 3781 TCTGTCTCCTCCCCCTCCCGCCCTTACCTCCAGGGAACCGCCCGC	QY 3841 TCGCACTTTGCCCCTGCTTGGCAGGGATAAAAGGGGGCTGAGGAAATACCGGACACGGT 3900 Db 3841 TCGCACTTTGCCCCTGCTTGGCAGCGGATAAAAGGGGGCTGAGGAAATACCGGACACGGT 3900	Qy 3901 CACCCGTTGC 3910 Db 3901 CACCCGTTGC 3910	RESULT 2 ABK94819 ID ABK94819 XX XX AC ABK94819; XX DT 29-AUG-2002 (first entry) XX DE Human stearoyl-CoA desaturase (SCD) control region. XX XX XX XX XX XX XX XX XX XX XX XX XX
OY 1981 ATACAAAAATTAGCTAAGTGGGGGATGCCTGTAATCCCAGCTACTTGGGAGGGT 2040	ATTTC ATTTC	21 IGTGCCACATGCCAAGTACTTCTGAGGCATGACTGGATGAGCTGTGCCACATCTGAAATCA 81 ICCAGTCTTGTTCAGAACTTTCACACGCACAGGGGGGGGAGGAGAGCTGGAATGCAGGACTTCACAGAATCTTCACACGACAGAGGAGGAGAAGCTTGAAATGAATTCACACGACAGAAGAAGAAGAATGAAT	2341 GGTCACTGGCCAGAGAGTTGGCCTTGAGACCAGTGGCCAACAAGAAGCTGCTT 2400 2341 GGTCACTGGCCAGAGAGTTGGCCTTGACCCTGAGACCAGTGGCCAACAAAGGAGCTGCTT 2400 2401 AGTCACTGGCCAGAGAGTTGGCCTTGACCCTGAGACCAGTGGCCAACAAAAGGAGCTGCTT 2400	401	61	521 521	2581 GGCTCCTACAGACACGGAAAAGATGGGGGCACAGGGACAGATCAGTAGGGTCAGAGGATC 2640 		GTTTCI - - - - GTTTCI	2751 TTCCATCTCTCCATATCTCTTTCTCACTTTAAAATGGAATAATGGGGTACCCACCTCC 2820 	821 CAGGGTCACAGAGAGG 	2881 AATACCTGCCAGCTATTCTATTCCACATCCAAGCCCTTTCGCCTGCTGGTGAAAA 2940 2881 AATACCTGCCAGCTATTCTATTCCACATCCAAGCCCTTTCGCCTGCTGGTGAAAA 2940 2881 AATACCTGCCAGTTTCCACAATCCAAAGCCCTTTCGCCTGCTGGTGAAAA 2940 2941 CACATGTCAGTGTTTCCTGACGTTTCCAAAAGAAGATTCCAAAATTACAACCTGCCAG 3000 2941 CACATGTCAGTGTTTCCTGACGTTTCCAAAAATTACAAACTTGCCAG 3000 3001 TCTGAAGAATCTCCAAAACATCCCGCACGCACCTGCCAGGATTCCAAAATTACAACCTGCCAG 3000 3001 TCTGAAGAATCTCCAAAACATCCCGCACGCATCCTGCAGGCGCGGCCTTCGGGATTGCGAC 3060

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dyslipidaemia; atherosclerosis; coronary artery disease; cerebrovascular disease; inflammation; cerebrovascular disease; inflammation; sinusitis; asthma; panorealitis; ostecarthritis; rheumatoid arthritis; acne; body weight disorder; obesity; cachexia; anorexia; psychiatric disorder; cancer; cystic fibrosis; pre-menstrual syndrome; diabetes; diabetic complication; genetic polymorphism; ds.
                                                                                                                                                                            Haardt M,
Nwaka SO;
                                                                                                                                                                          Knickle LC,
Jenkins DK,
                                                                                                                                                                                                                                                           Claim 23; Fig 26; 225pp; English.
                                                                                                                     19-NOV-2001; 2001WO-CA001632.
                                                                                                                                       17-NOV-2000; 2000US-0248589P.
                                                                                                                                                        (XENO-) XENON GENETICS INC
                                                                                                                                                                          Goldberg YP,
De Antueno RJ,
                                                                                                                                                                                                     WPI; 2002-508327/54.
                                                                                WO200240666-A2
                                                                Homo sapiens
                                                                                                    23-MAY-2002
                                                                                                                                                                           Winther MD,
                                                                                                                                                                                    Ponton A,
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Allen SJ;

The invention describes an isolated polypeptide segment (I) whose genes

are fat regulated. (I) or the polymuclectide encoding it (II) are useful

for diagnosing the presence of or a predisposition for a disorder

containing flip or circulated genes in a subject. A composition

containing (I) or (II) is useful for treating a disorder involving fatty

containing (I) or (II) is useful for treating a disorder involving fatty

containing (I) or (II) is useful for treating a disorder involving fatty

cold regulated genes, where the disorder, escama, cardiovascular

disorders (such as hypertriglyceridemia, dyslipidaemia, atherosclerosis,

coronary artery disease, cerebrovascular disease or peripheral vascular

discase), inflammation (such as sinusitis, askima, pancreatitis,

coronary artery disease, cerebrovascular disease or peripheral vascular

coronary artery disease, cerebrovascular disease or peripheral vascular

coronary artery disease, cerebrovascular disease or peripheral vascular

coronary artery disease, cerebrovascular disease, postreatis,

corpolications, remember as sinusitis or acne), body weight disorders

complications. (I) or (II) is useful as research agent and materials for

discovery of treatments and diagnostics for a disease, particularly human

coronary action genetic polymorphism, for detecting changes in the level of

corporating genetic polymorphism, for detecting changes in the level of

control region from a gene encoding a fatty acid regulated protein Novel isolated polypeptide segment encoded by fat regulated genes, useful for diagnosing the presence of or a predisposition for a disorder involving fatty acid regulated genes in a subject.

Sequence 1970 BP; 428 A; 590 C; 588 G; 364 T; 0 U; 0 Other;

بن ب 2180 CAGAGAGAACCTGAAGGGGGTCAGACCACGTACAGATTTCTGTGCCACATGCCAAGTACT 2240 TCTGAGGCATGACTGAGGAGCTGTCCACATCTGAAATCATCCAGTCTTGTTCAGAACTT 2300 TCACACCGGACAGGGAGCCAGGACTGGAATGCAGTCTCCTGGTCACTGGCCAGAGAGTTG 2360 2361 GCCTTGACCCTGAGACCAGTGGCCAACAAAGGAGCTGCTTAGTCTACCTCCCAGGAAATC 2420 CAGAGAGAACCTGAAGGGGGTCAGACCACGTACAGATTTCTGTGCCACATGCCAAGTACT 120 rcreaecearcacreaerereceacarcreaaarcarccacrerrerreaeaacrr 9 Gaps 44.8%; Score 1751.8; DB 6; Length 1970; 99.7%; Pred. No. 0; ive 0; Mismatches 2; Indels 3; 3; 2; Indels Matches 1786; Conservative Similarity 61 2241 2181 121 2301 181 Local à ò g à g ò g

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The present sequence is that of the promoter region of the human stearoyl cof desaturase-1 (hSCD1) gene. The promoter structure is similar to that cof the mouse SCD1 promoter and contains conserved regulatory sequences of the human SCD1 promoter and contains conserved regulatory sequences for the binding of several transcription factors. Like the mouse SCD1, colesterol at the level of gene transcription. The sterol regulatory clement binding protein (SREBP) plays a role in the transcriptional clement binding protein (SREBP) plays a role in the transcriptional clements that modulate and control SCD1 expression in humans, and to clements that modulate expression of SCD1 in humans. The invention clements that modulate expression of SCD1 in humans. The invention clements of sorders or conditions relating to serum levels of triglyceride, very lipoprotein, total cholesterol, or production of secretions from memoranes, monounsaturated fatty acids, wax esters, etc. Methods for membranes, monounsaturated fatty acids, wax esters, etc. Methods for are also provided. These disorders include various skin diseases and diseases, and immune disorders as well as cholesterol disorders include various skin diseases, eye limidamiae and cantillus hypertension, neurological diseases, eye limidamiae and cantillus hypertension, neurological diseases, eye limidamiae and cantillus hypertension, neurological diseases, eye limidamiae and cantillus hypertension, neurological diseases, eye limidamiae and cantillus such estators as well as cholesterol disorders, eventual expensions and cantillus and an expension of an enditory and and an expension and cantillus such as cancer and multiple sclerosis, non-insulin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3459 CCCAGCCCTTCCAGAGAAAAGCTCCCGACGCGGATGCCGGGCAAGGCCCAGCGGCG 3518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying an agent for treating disorders related to serum levels of fatty acids and glycerols, by contacting screening assay with delta-9 stearcyl-CoA desaturase activity with compound and measuring the activity.
                                                                                                                                           "CCAAT enhancer binding protein-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CCCGCCCCTTCCAGAGAGAGACTCCCGACGCGGGATGCCGGGCAGAGGCCCAGCGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 617 BP; 117 A; 211 C; 205 G; 84 T; 0 U; 0 Other;
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                     '*tag= h
/bound_molety≈ "nuclear factor y"
404. .408
                                                                                             "nuclear factor 1"
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11.5%; Score 450.4; DB 5;
Best Local Similarity 99.8%; Pred. No. 7.9e-83;
Matches 451; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ntambi JM,
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                                                                                                                                                                                                                                                                                                                                                                                             (XENO-) XENON GENETICS INC.
(WISC ) WISCONSIN ALUMNI RES FOUND.
(UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Page 83; 130pp; English.
                                                                                                                         /*tag= j
/bound_moiety= "(
(C/EBP-alpha)"
467. .474
/*tag= k
                                                                                         /bound_moiety=
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2000US-0255771P.
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                                                     protein bind
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15-DEC-2000;
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Miyazaki M;
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CCCAGCCCCAAACCGGGTCCCCAGCCCCTTCCAGAGAAAAGCTCCCGACGCGGGATGCC 1378
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/bound_moiety= "sterol regulatory element binding protein
(SREBP)"
                                                                AGCGAGGAGCTGGCGGCAGGGAACAGCAGATTGCGCCGAGCCAATGGCAACGGCAGGA
                                                                                                                           CGAGGTGGCACCAAATTCCCTTCGGCCAATGACGAGCCGGAGTTTACAGAAGCCTCATTA
                                  GGGCAGAGGCCCAGCGGGGGGGAAGAGAGAAGCTGAGAAGGAGAAACAAGAGGGGGG
                                                                                                                                                                                                                                      3680 GCATITICCCCAGAGGCAGGGCAAGGGCAGGACAGGGTGGTGGTGGTGTGGTGTGTGGTGTGTGGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stearoyl-CoA desaturase-1; hSCD1; SCD1; human; promoter; screening; assay; triglyceride; very low density lipoprotein; high density lipoprotein; low density lipoprotein; cholesterol; muccus membrane; fatty acid; wax ester; anticholesterolemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95. .103
//tag= a
/bound moiety= "SP1"
102. .169
//tag= b
//tag= b
//tote= 'Polyunsaturated fatty acid response region"
                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCAGCGGATAAAAGGGGGCTGAGGAAATACCGGACACGGTCACCCGGTTGC 3910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human stearoyl-CoA desaturase-1 gene promoter region.
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/bound moiety= "nuclear factor 1"
176. .180
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'bound_moiety= "SP1"
[31, .140
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14-AUG-2000; 2000US-0225757P.
14-AUG-2000; 2000US-0225759P.
18-AUG-2000; 2000US-0226279P.
22-AUG-2000; 2000US-0226868P.
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22-AUG-2000; 2000US-0227182P.
23-AUG-2000; 2000US-022709P.
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01-NOV-2000;
     3579 AGGGAACAGCAGATTGCGCCCGAGCCAATGGCAACGGCAGGACGAGGTGGCACCAAATTCC 3638
                                                                                                         3639 CTTCGGCCAATGACGAGCCGGAGTTTACAGAAGCCTCATTAGCATTTCCCCAGAGGCAGG 3698
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64 GGTGGAAGAAGATGAAGAAGGAGAAACAGAGGGGAAGGGGAGCGAGGAGCTGGCGGCAG 123
                                                                   124 AGGGAACAGCAGATTGCGCCGAGCCAATGGCAACGGCAGGACGAGGTGGCACCAAATTCC
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                                                                                                                                                                                                                                                                                                                                                                                                    CTGAGGAATACCGGACACGGTCACCCGTTGC 3910
                                                                                                                                                                                                                                                                                                                                                                                                                            CTGAGGAAATACCGGACACGGTCACCCGTTGC 455
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24-FEB-2000; 2000US-0180628P.
22-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-018350P.
15-MAR-2000; 2000US-0189374P.
17-MAR-2000; 2000US-0199074P.
19-MAY-2000; 2000US-020515P.
07-JUN-2000; 2000US-020515P.
07-JUN-2000; 2000US-021513F.
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07-JUL-2000; 2000US-021688P.
11-JUL-2000; 2000US-0217496P.
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11-JUL-2000; 2000US-0217496P.
14-JUL-2000; 2000US-02218290P.
26-JUL-2000; 2000US-0221829P.
14-AUG-2000; 2000US-022451BP.
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08-NOV-2000; 2000US-0246611P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249208P.
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17-NOV-2000; 2000US-0249211P.
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(HUMA-) HUMAN GENOME SCI INC.

Ruben SM; Rosen CA, Barash SC,

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 38065; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91221. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to cyplucleotides may be used to production of (I). Additionally, (I) cyplurcleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and oulturing the cell to express the proteins and polynucleotides may be used to prevent, cancers and cancer metastases of haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 concers from the present invention. AAK54942 to AAK54950 and AAM82169 very represent suggestion the exemplification of the present invention.

Sequence 8880 BP; 2388 A; 1807 C; 1844 G; 2841 T; 0 U; 0 Other;

16; Query Match 9.9%; Score 386; DB 4; Length 8880; Best Local Similarity 54.7%; Pred. No. 2.5e-69; Matches 1194; Conservative 0; Mismatches 850; Indels 138; Gaps

λŏ	14 TITAAATCATACAATTTAATGGCTTTTAGTATATTCACAG-GTTGTGCATCCATCAC 69
dd	
ò	70 AATCCATTTAGAACAGTTTTATTACTCGAAAATAAACCTGGATTCCTTAGCCATCAC 129
οp	6197 CATCAAGTTTAGAACATTTTTATAACCCCAGAAAGAAACCCTGTAGCTTTAGCTGTCAC 6256
à i	30 CCCCAAGATCTCCTCCTTCCAGGCAACCCACCAATCTACTTTCTGT 18
a a	6257 CTTCCAGTACCACTTTCTTCTCCCCTTTCCCCTAGGCTATCACTAAAACTTTCTGT 6316
λò	188 CTCTATAAATTTGCCAATTCTGGACATTTCATATAAATGGAAGGAA
qq	6317 CTATATAGATITGCCTATTCTGGACATTTCATATAAATGGAATCATATAATAGTGGCCT 6376
δ	248 TITGIGACTGGCTGCTTTCACTTAGCALTCTATTTTAAGGCTCA-TTATGTTACAGTAC 306
QQ	4
δy	366
qq	6437 GTATCAGTGTTTTGTTTTGTTTTGCAGACGGAGTTTTGCTC 6482
<i>\</i> 0	367 TCATATTATTAGAGACAGGTTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGCACAATC 426
qq	6483
ò	427 ATAGCICACIGIAACCICAAACICCIGGGCICAAGIGAICCIACCICAGCCICCAGA 486
Db	6515 TIGGCICACTGCAACCTCTGCGCTTCAAGTGATTCTCCTGCCTCAGCTCCGGA 6574
δλ	487 GIAGGIAGGACTACAGGCACACACACACATACTOGCTAATTTTTTTTTAATTTTCAT 546
QQ	6575 ATAGCTGGGATTACAGGTGCACCATGCCCAGCTAATTTTGTACTTTCAGTACACA 6634
δ,	547 TITARGIAFICATTTTCTTTCTTTTTGTTGTTGTTGTTTGAGA 591
Db	CAIGITGGCCAGGCTAGICTITITITITITITITITITITITITITITITITAGA 6
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δγ	650 CTIGACTICCIGGGCTCAAGTGCTCCTCCTGCCTCCAGGCTCCCAAGTAGCTGGGACTACA 709
qq	6755 CTCCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCCCGAATAGCTGGGACTACA 6814
ζ	710 AACACGIGICACCAIGCCIGAIAIIITIIIITCIIGAAACAGGIAICACA 763
d d	6815 GGCGCTGCCACCGCGCCCGGCTAAITITITAGTATITITAGTAGAGGACGGGGTTTCACC 6874
č	764 CIGITGCCCAGGCTGGAGTACAGTGGGGGTAATAATAGCTCACTGCAGGCTCCCCTCCTGG 823
qq	6875 GIGITAGCCAGGAIGGICTCGAICTCCTGACCICGTGAICCACCGCCTCGCCT
٥'n	824 GCTCAAGCAATCCGCTGGCCTCAGCATCCTGAGTAGCTGGGACTACAGGCTTGTGCCACC 883
Db	6935 AGIGCTAGTATTACAGGCTTGAGCCACGGGCCCGGCCAGGCCAGGCTAGTCTTGAACTCC 6994
λŏ	884 AGGCCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
ΩP	70
δγ	944 AGGCTGTATTTTTATTGTTGAGACAAGGTCTCACTATGTTGCCATGATCCCCCCACCTCC 1003
Dp	7055 ACCATGCCCGGCTGCAGTTTTATTCCTTTTTGTTGCTGAATAGTATCTCATTTTATGG 7114
òy	1004 ACTICCCAAAGTGCTCATCTTATCTGTTCATTAGTCAGTTGACAGACA
qq	7115 ACATACTCATATTTTATGCATTCATTTGTCAGCTAATAGACATTTGGGTAACTT 7168

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The invention relates to genes and their expression profiles are used for: (a) screening modulators of precursor stem cell differentiation into osteoblasts, or bone tissue deposition; (b) diagnosing abnormal rate of osteoblast formation or deposition of bone tissue, abnormal rate of osteoblast formation or cled in (b), or monitoring the progression of bone tissue deposition. Specific conditions include postmenopausal osteoporosis, glucocorticoid osteoporosis or male osteoporosis, osteoporosis, glucocorticoid osteoporosis or male osteoporosis, osteoporia, osteodystrophy, drug-cinvolve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), skeletal disease linked to breast cancer, mastcoytosis, Fanconi syndrome cor fibrous dysplasia. The present sequence is that of an osteoblast differentiation associated cDNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO car fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation process.
                                                                                                                                                                                                                                                           Human; osteoblast; stem cell differentiation; bone tissue deposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 ATCATATTATAGAGACAGGTTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGCACAAT
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55.4%; Pred. No. 6.3e-67;
tive 0; Mismatches 726; Indels 115; Gaps
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                                                                                                                                                                                                                       Human osteoblast differentiation related cDNA SEQ ID NO 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 3; 78pp + Sequence Listing; English.
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8193 AAAAAAAAAAAAAGAAAA 8214
                                                                                                               ABQ88096 standard; cDNA; 92638 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENE LOGIC INC.
(PROC ) PROCTER & GAMBLE CO.
                                                                                                                                                                                   18-SEP-2002 (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  WO200250301-A2.
                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                 ABQ88096;
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Mertz L;
                                                                                            ABQ88096/
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کر ط	486 AGTAGCIAGGACTACAGGCACACAGCCATACCIGGCIAATITITITITAAITITCA 545	<i>ò</i> €	1501 TGATCTCCAGCTCACTGCAACTTTCGCCTCCCC	030CTCCC
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	57760TTCTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCT 57714	qq	56694 CCCGAGTAGCTGGGACTACAGGCGCCCGCCAC	
		<i>\$</i> 8	1621 TAGAGATGGGATTTCACTTTGTTGGCCAAGCT	GCCAAGC GCCAGGAT
	664 CTCAAGTGATCCTCCTGCCTCCCAAGTAGCTGGGACTACAAAAACACGTGACGT 723	8 8	1670TGTCATAATTGTTGTAACTATTGTTCCT	ATTGTTCC:
	5/853 ILCAGGCCACTATCICCTGCCTCCGGGGTAGCTGGGGCTACAGGGGCCCACCATCA 57594 724 TGCCTGGCTGATATTTTTTTTTTGAAACAGGGTATCACTCTGTTGCCAGGCTG 778	₹ <i>&</i>	1726 AAAAITAAATCTTAGAATCCAAATCAGTGTGTGTTAC	GGGATTA(CAGTGTGT
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	779 GAGTACAGTGGCGTAATAAGCTCACTGCAGCCTCCCCTGGGCTCAAGCAATC 835	<i>à</i> ∄	1786 CAGIGIGACCAGGCCTCAGGAGTAGAGGIGA	AGAGGTG
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	CAGGGGAAGAAAACTTGGGAAAATGAAGCATGTTTAGAAATCAGCAAGAGTGCAGG	K K	AAK69044;	
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	1261 GTTTTTCGGAGTTTTATTTTATTTCTGTTGAAATGTGCAGTTTGATGAAGAAAA 1320	X 6 X	Human immune/haematopoietic antigen	an genomi
	19259 IGACIIIGAICACCIGAGGIAAACTITGGCAGACTICTCCATTGTAAAGTTACTCT 56934 1321 TTATACTAAGTGAGAAGTGAGAATTAAGGCTGGAATAAGGGCGTTCAGAAGAAAAAAAA	K K K	<pre>Human; immune; haematopoietic; immune/haem cytostatic; gene therapy; vaccine; metasta</pre>	nne/hae metast
		SX	Homo sapiens.	
	1381 AGCACTTTGAATACCAAAATTAAGGAGCTTGGCTGTAAACAAAATAATAAAAAAATACACAA 1440	N X	WO200157182-A2.	
	56873 AGAATTGGGGA-ATTATGTTCTACCTCCTTAAGGGCAGAATATCTACACAGGTTTTTGTT 56815	G ¥	09-AUG-2001.	
	1441 TTTTTTTTTTTGGAAAGAGTCTTGCTCTTCACCCTGGAGGGCAGTGGTG 1500	PF	17-JAN-2001; 2001WO-US001354.	
	56814 TTTTTTTTTTTTTGAGATGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCCA 56755	7. P. P. P. P.	31-JAN-2000; 2000US-0179065P. 04-FEB-2000; 2000US-0180628P.	
		:	CA-FED-GOOV, COUCUS-UIDAGOAF.	

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ACCATGCCCAGCTGATTTTGTATTTTAG 1620
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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30-AUG-2000;
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marker, W3440 and an STS marker, ADCYAP1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  The present genomic sequence is that of human pituitary adenylate cyclase activating polypeptide (PACAP). This gene is localised to the short arm of chromosome 18p11 and synthesised in the retinal ganglion cells. The gene missed that is isolated from lymphocytes of individuals. The coding region of the gene has a dinucleotide repeat polymorphism marker known as W1440 and am STS marker, ADCYAP1 is located in the 3'UTR. These markers are useful to map the gene physically and genetically to the chromosome 18. This sequence can be used to design probes for detecting the presence or absence of a mutation in the wild type PACAP gene. It is also useful for genetic diagnosis of neuropsychiatric disorders like bi- polar affective disorder(BP-I) and schizoaffective disorders like bi- polar which are more valid than current clinical diagnosis based on clinical observation and subjective reports. It is used for identifying compounds that modulate PACAP gene expression which are useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATGIGGATCACCTGAGGTCAGGAGTTCAAAACCAGCCTGGCCAACATGGTGAAAACCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGGCAGTGGTGATCTCAGCTCACTTGCAACTTTCGCCTCCCGGGTTCAAGCAATTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTACAATGGCATGTTCTCAGCTCACCTCTGCCTCCGGGCTCAAGCAATTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 84607 BP; 23055 A; 17765 C; 18980 G; 24744 T; 0 U; 63 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                 Use of a gene linked to the region of a chromosome associated with neuropsychiatric disorders, especially for diagnosis of bi-polar affective disorder and schizoaffective disorder manic type.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 356.2; DB 2;
Pred. No. 5.5e-63;
); Mismatches 233;
                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2A-2U; 99pp; English.
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MILLENNIUM PHARM
UNIV CALIFORNIA.
                                                                                                                                                                    WPI; 1999-611046/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1549
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(MILL-) (REGC ) 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3895 ACCTAGCCCTGATTTTTCAAGACAAACTGAAAACTGGATTTAGATGTGAAATCTTTTTT 3954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             729 GOCTGATATTTTTTTTTTGAAACAGGTATCACTCTGTTGCCCAGGCTGGAGTACAGTG 788
                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an antisense compound 8 to 30 nucleobases in length targetred to a nucleic acid encoding glycogen synthase kinase 3 alpha. The antisense compound specifically hybridises with and inhibits the expression of glycogen synthase kinase 3 alpha. The antisense compound is useful for the treatment of a diseases associated with glycogen synthase kinase 3 alpha such as diabetes, a neurological disorder, a haematopoietic disorder, a hyperproliferative disorder or a developmental disorder. The antisense compounds may also be used prophylactically to prevent or delay infection, inflammation or tumour formation. The present genomic DNA sequence encodes human glycogen synthase kinase 3 alpha protein
                                                                                                                                                                                                                                                                                                                                Antisense compound 8 to 30 nucleobases in length comprising a compound that its targeted to a nucleic acid molecule encoding glycogen synthase kinase 3 alpha, useful for the treatment of e.g. diabetes and hyperproliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         550 ATGIATICATTITCTTICTTITTTGTTGTTGTTTTGAGATAGGGTCTCACTTTGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12394 BP; 2780 A; 3043 C; 3547 G; 3024 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.9%; Score 349.8; DB 4; Length 55.2%; Pred. No. 7.3e-62; ive 0; Mismatches 742; Indels
                                                                                                                                                                                                                                                         Wyatt JR;
                                                                                                                                                                                                                                                                                                                                                                                                           Example 15; Page 92-100; 115pp; English.
                                                                                                                                                                                                                                                         Butler MM,
                                                 u
.11786
                              .11712
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                                                                                                                                                                                               21-JAN-2000; 2000US-00488856.
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Best Local Similarity 55.2
Matches 1016; Conservative
10431.
/*tag=
10524.
/*tag=
11713.
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                                                                                                         WO200152865-A1
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                                                                       20625 ACTCGGGAGGCTGAGGCAGAATGGCGTGAACCCGGGAGGCGGAGCTTGCAGTGAGCC
                                             2029 ACTTGGGAGGGTGAGGCAGGAGATTTCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGC
                                                                                                         2089 GAGATCACACCACTGCACTCCAGCCTGGGGGAGAGAGGGGAGTTTCCTCTCAAAAAACA
               product= "Human glycogen synthase kinase 3 alpha"
                                                                                                                                                                                             20745 AAAAAAAAAAAAAAAAAGGAATCATACTTGGAAAGGGAA 20785
                                                                                                                                                                  2149 AAAAACAAAAGAATTAAGCAAATTAGACATTGCAGAGAGA 2189
                                                                                                                                                                                                                                                                                                                                                               Human glycogen synthase kinase 3 alpha genomic DNA
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115. 11786
/*tag= a
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5639. FT
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2438. .2625
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398. .2437
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8228.
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TCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGATCACACCCTGCACTCCAGCCT 2114
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         1844 AAAATATTCTCCGGGCCAGGCGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAAGGC
                                                                                                                                                                                       TCAAAACCAGCCTGGGCCAACATGGTGAAACCCCGTCTTATAAAAATACAAAAATTAG
                                                                                                                                                                                                                 5080 TTTIAAGIGGGGGGGGGGGGGGGGGCTGTCACGCCTGTAATCCCAGCACTTTGGGAGGC
                                                                                                   ---CCTGAGGTCAGGAGT
                                                                                                                                           CTAAGTGGTGGCGCATGCCTGTAATCCCAGCTACTTGGGAGGGTGAGGCAGGAAATT
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2000US-0225270P.
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2000US-0184664P.
2000US-0186350P.
2000US-0189874P.
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2000US-0205515P.
2000US-0205467P.
2000US-0214886P.
2000US-0215135P.
2000US-0215135P.
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2000US-021680F.
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2000US-0218290P.
2000US-0220963P.
2000US-0220964P.
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2000US-0224519P.
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17-MAR-2000;
18-APR-2000;
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28-JUN-2000;
30-JUN-2000;
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11-JUL-2000;
11-JUL-2000;
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26-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
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TAGAGATGGGATTTCACTTTGTTGGCCAAGCTGGTCTCAAACTTTTTGCTGTCTAAATTG 1680
            3805 TACAGAIGGGGTTTCACCAIGTIGGTCAGGCTGGTCTCGAACTCCTGACTTCATGAICCG 3864
                                                                                                                                                                           Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic; gene; ds.
                                                                                                3921 ---GCTAATTTATTTTTTTGTACAGAGTTTCTCCATGTTGCCCAGGCTGATCTGGAA
                                                                                                                                                                                                                                                                                                                                              AATCCAAATCAGTGTTGGTTTGACCACTGTCACTTGAGAACCACAGTGTGACCAGGGGC
                                                                                                                        CTCAGGAGTAGAGGTGATCTCTGCTCGAAAGAGAAATAGAATGAAAATATTCTCCGGGCC
                                                                                                                                                               AGGCGTGGTGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCATGTGGATCAC
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2000US-0189874P.
2000US-0190076P.
2000US-0198123P.
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02-MAR-2000;
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19-MAY-2000;
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                                                                                                                                                                                                                                                                        3805 TACAGATGGGGTTTCACCATGTTGGTCAGGCTGGTCTCGAACTCCTGACTTCATGATCCG
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                                                                                         1441 TITITITITITITITIGAGAAGAGTCTIGCICTTICACCCTGGCTGGAGGGCAGTGGTG
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                                                                                                                                                                       3685 cdarcrcadcrcacracaaacrccaccrccadgerrcaadaarrcrccrccrradcr
         Sequence 13216 BP; 3041 A; 3400 C; 3243 G; 3532 T; 0 U; 0 Other;
                                    Length 13216;
                                    Score 349; DB 4; Length 13 Pred. No. 1.1e-61; 0; Mismatches 210; Indels
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                                    Query Match
Best Local Similarity 70.0%;
Matches 516; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
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2000US-0249214P

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              2000US-0241787P.
2000US-0241808P.
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2000US-0246474P.
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2000US-0246610P
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2000US-0249207P
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2000US-0256719P.
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                                       20-OCT-2000;
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01-NOV-2000;
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AAL05121 standard; DNA; 29163
                       AAL05121;
1244 TCAGCAAGAGTGCAGGGGTTTTTCGGAGTTTTTATATTTCTGTTGACAAATGTGCAG 1303
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                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated mucleic acid molecule (I) comprising a mucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the selecting a composition for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 TCAGCAAGAGTGCAGGGGTTTTTCGGAGTTTTTATTTTTATATTCTGTTGACAATGTGCAG
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98.9%; Pred. No. 5.9e-62;
tive 0; Mismatches 4
                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                          Claim 1; Page 10183; 11750pp; English.
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                                                                                                                          2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
                                                                           20-FEB-2001; 2001WO-US005171
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13-DEC-2000; 2000US-0255281P-
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                               MO200160860-A2.
                                                                                                                           25-MAY-2000;
       Homo sapiens
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RESULT 13 AAL05121

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reproductive system related antigen; reproductive system disorder;
                      Human reproductive system related antigen DNA SEQ ID NO: 7809.
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2000US-0232398P.
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AGGCGTGGTGGCTGTGTAATCCCAGCACTTTGGGAGGCCAAGGCATGTGGATCAC 1920
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                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
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      2160
    disorder;
                                                                                 Human; testicular antigen; testes; cancer; metastasis; immune disorde: reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                               Human testicular antigen encoding DNA fragment SEQ ID NO: 2665.
                                                                                                                                                                                                                                                                                                   ABL98013 standard; DNA; 29163 BP
                                                                                                                                                               ATTAAGCAAATTAGACA 2177
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1861 AGGCGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCATGTGGATCAC
                                                                                                                                                                              4033 GGGTGCGGTGCCTCACGCCTGTAATTCCAGCACTTTGGGAGGCCAAGGCAAGGTGGATCAG
                                                                                                                                                                                                                                                                                                                                                                            GAGGCAGGAGAATTTCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGATCACACCA
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                                                                                                                                                                                                                                                                                                  1981 ATACAAAAATTAGCTAAGTGTGGTGGCGCATGCCTGTAATCCCCAGCTACTTGGGAGGGT
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ID AAS42014 standard; DNA; 6437 BP.
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2000US-0214886P.
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2000US-0184664P.
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2000US-0190076P.
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2000US-0217496P.
2000US-0218290P.
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24-FEB-2000;
02-MAR-2000;
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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28-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1501 TGATCTCAGCTCACTGCAACTTTCGCCTCCCGGGTTCAAGCAATTCTCTCTGCTTCAGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1741 AATCCAAATCAGTGTGTTGGTTTGACCACTGTCACTTGAGAACCACAGTGTGACCAGGGC
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                                                     17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
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17-NOV-2000; 2000US-0249244P.
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14-AUG-2000; 2000US-022521BP.
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Rosen CA, Barash SC, Ruben SM

WPI; 2001-465566/50.

Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.

Disclosure; SEQ ID NO 2140; 1180pp; English.

The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the CDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperpoliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. Alzbeimer's disease), metabolic arthritis), neurological disorders (e.g. Alzbeimer's disease), metabolic cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the

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invention can also be used in gene therapy. AAS41685-AAS42192 represent DNA sequences encoding for the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 56.7%; Pred. No. 2.4e-61;
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(c) 1993 - 2004 Compugen Ltd.
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APPLICANT: Brett P. Monia
APPLICANT: Robert McKay
APPLICANT: Robert McKay
APPLICANT: Adeline W. Butler
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXPR
TITLE FEBRENCE: RTS-0115
CURRENT APPLICATION NUMBER: US/09/488,856A
CURRENT PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 88
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Pred. No. 5.9e-77;
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; Sequence 10, Application US/09488856A
; Patent No. 6316259
; GENERAL INFORMATION:
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NAME/FEY: misc_feature
LOCATION: (1)...(84495)
OTHER INFORMATION: n = A,T,C or (9-797-906-3
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1935 TCAAAACCAGCCTGGCCAACATGGTGAAACCCCGTCTACTAAAAATACAAAAATTAG
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                                                                                                                                 .7334 ATTACAGGTGGCGCCCACCATGCCTGGCTAATTTTTGTACTTTTAGCAGAGACGAGTTT
                                                                                                     Bandyopadhyay, Paramita
Roy-Chowdhury, Jayanta
TITLE OF INVENTION: Hepatocellular Chimeraplasty
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
STREET: 300 Pheasant Run
CITY: Newtown
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; sequence 3, Application US/09108006C; Patent No. 6524613; GENERAL INFORMATION:
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US-09-108-006C-3/c
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                                                                        445 AAACTCCTGGGCTCAAGTGATCCTACCTCAGCC-TCCAGAGTAGCTAGGACTACAGG
                                               Gaps
                                               85;
                Score 345; DB 4; Length 84495;
Pred. No. 2.6e-75;
0; Mismatches 715; Indels 85
                        Query Match
Best Local Similarity 55.0%;
Matches 979; Conservative
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                                                                                                                18461
                                                                                                                                              504
                                                                                                                                                                         18401
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1456 TCCCAGCCAGGTGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGATCGAAACGGG 1397
                                                                                 1396 CAGATCACCTGAGGTCAGGAGTTCCAGACCAGCCTGGCCAACATGGTGAAAACCCCGTCTC
                                                                                                                                                   1973 TACTAAAAATACAAAAA-TTAGCTAAGTGTGGTGGCGCATGCCTGTAATCCCAGCTACT
                                                                                                                                                                                  2032 TGGGAGGGTGAGGAGAATTTCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAG
                                                                                                                                                                                                                                                                                      1913 IGGAICACCIGAGGICAGGAGIICAAAACCAGCCIGGCCAACAIGGIGAAACCCGGICIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: KOHN & ASSOCIATES
STREET: 30500 No. 6025183thwestern Highway, Suite 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 48334

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other nucleic acid /desc = "Cosmid including ACHE promotor, ACHE gene and ARS gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Montgomery, llene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELEPHONE: (248) 539-5050
TELEPHONE: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
FILING DATE:
CLASSIPICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08814095
Patent No. 6025183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 30500 No. 60251
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7q2
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2152 AACAAA 2157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1156 CÁACÁÁ 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1506 TCAGCTCACTGCAACTTTCGCCTCCCGGGTTCAAGCAATTCTCCTGCTTCAGCCTCCCAA 1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTAGCTGGGACTACAGGCACTTCCCACCATGCCCAGCTGATTTTTGTATTTTTAGTAGAG 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCGGGCCAGCGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCATG 1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1876 Transratinaraaksassichrischerenereksassissassissassissassassissas 1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1816 Argéricacrécaaccrigaccricigéscricaaccaricerecrecreserente 1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1756 GTAGCTGAGAGCACAGGTGTGGGCACCATGCCTGGCTAATTTTTGTATTTTTAGTAGAG 1697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1696 ACAGGGTCTCACTATGTTGCCCCAGGCTGTTGAACTCCTGGGCTCAAGTGATCCTCCC 1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1674 AIAATTGTAACTATTGTTCCTTTTGCTGAGGTAGGCCCCCAGACCAAAAAAATAA 1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1636 ACCTIGGCCTCCCAAAGIGCTGGGATTACAGGGTGAGCCACCGGCCCAGCGGAAAAGCA 1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1734 ATCTTAGAATCCAAATCAGTGTGTTTGACCACTGTCACTTGAGAACCACAGTGTGA 1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1576 TGTATTGAGTGTCCTTGTGTGCCCCAGGCAGGCTGTGTGGGGGGTGATGAAGA 1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1794 CCAGGGCCTCAGGAGTAGAGGTGATCTCTGCTCGAAAGAGAAAATAGAAATAAAATAT-TC 1852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1516 TCACAGCTGCCCCGTGTCTGGTATTCACTATCTGCCTGCAATGCATTAGAAACCTCTAAC 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.2%; Score 322.4; DB 4; Length 3805; llarity 68.3%; Pred. No. 2.2e-70; Conservative 0; Mismatches 216; Indels 14;
OPERATING SYSTEM: DOS SOCTAMER: TSASEGO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,006C FILING DATE: 30-Jun-1992
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                           APPLICATION UNMERS. 60/054,288
FILING DATE: 30-APR-1997
APPLICATION NUMBER: 60/054,837
FILING DATE: 05-AUG-1997
APPLICATION NUMBER: 60/064,996
FILING DATE: 10-NOV-1997
APPLICATION NUMBER: 60/074,497
FILING DATE: 12-FEB-1998
APPLICATION NUMBER: 60/074,497
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: FLIEDENT INFORMATION:
REFERENCE/DOCKET NUMBER: 2928
REFERENCE/DOCKET NUMBER: 7991-015-999
TELECOMMUNICATION INFORMATION:
TELEPRAKE 215-504-4444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1626 ATGGGATTTCACTTTGTTGGCCAAGCTGGTCTCAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOCATION: 71...114
COTHER INFORMATION: Exon 1
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-108-006C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3805 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Best Local
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FEATURE:
NAME/KEY: exon
LOCATION: 24090.25177
LOCATION: 24090.25177
LOCATION: 24090.25177
LOCATION: A control of translation start:
OTHER INFORMATION: / function= "(translation start:
OTHER INFORMATION: / evidence= EXPERIMENTAL
OTHER INFORMATION: / gene= "ACHE"
FEATURE:
NAME/KEY: exon
LOCATION: 25524.26009
LOCATION: 25524.26009
LOCATION: 25524.26009
LOCATION: 7646ance= EXPERIMENTAL
OTHER INFORMATION: / evidence= EXPERIMENTAL
OTHER INFORMATION: / gene= "ACHE"
OTHER INFORMATION: / gene= "ACHE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: complement (34528..34895)
OTHER INFORMATION: /function= "arsenite resistance OTHER INFORMATION: gene"
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /gene= "AR"
                      LOCATION: 4089..22464
OTHER INFORMATION: /function= "ACHE Promotor"
OTHER INFORMATION: /standard_name= "ACHE Promotor"
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NAME/KEY: exon
LOCATION: 22465.22537
OTHER INFORMATION: /function= "non-translated"
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /mumber= 1
FEATURE:
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LOCATION: 27005..27274
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene="ACHE"
OTHER INFORMATION: /number= 4
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LOCATION: 27255..28007
IDENTIFICATION METHOD: experimental
OCHBR INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /gene= "ACHE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 28008..28129
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence=EXPERIMENTAL
OTHER INFORMATION: /gene="ACHE"
OTHER INFORMATION: /number= 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: complement (33779..33963)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon complement (33493..33591)
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: terminator
LOCATION: 28129..28131
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: terminator LOCATION: 27385.27387
NAME/KEY: promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
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FEATURE:
NAME/KEY:
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NAME/KEY:
LOCATION:
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1505 CTCAGCTCACTGCAACTTTCGCCTCCCGGGTTCAAGCAATTCTCCTGCTTCAGCCTCCCA 1564
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                                                           NAWE/KEY: exon
LOCATION: complement (33297..33408)
OTHER INFORMATION: /géne= "AR"
OTHER INFORMATION: /number= 5
FEATURE:
NAWE/KEY: exon
LOCATION: complement (32959..33094)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
FEATURE:
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NAME/KEY: exon
LOCATION: complement (31363..31534)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: complement (31131..31284)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: complement (30816..31011)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: complement (30187..30274)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number='14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: complement (29945..30073)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: complement (29664..29856)
COTHER INFORMATION: /gene= "ARS"
COTHER INFORMATION: /number= 16
                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: complement (32569..32628)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 7
                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: complement (32386..32468)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: complement (31894..32080)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: complement (30470..30626)
OCHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
/gene= "AR"
/number= 4
OTHER INFORMATION:
OTHER INFORMATION:
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NAME/KEY: exon
LOCATION: compl
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NAME/KEY: exon:intron junction
LOCATION: (348578)...(348579)
OTHER INFORMATION: exon 10:intron 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (195242)...(195341)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: unsure
LOCATION: 202703
OTHER INFORMATION: unknown
NAME/KEY: misc_feature
LOCATION: (202771)...(202870)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (206246)...(215602)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (218126)...(218225)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (230157) ... (230256)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (232299) ... (232398)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (236552) ... (236651)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (236789) ... (248788)
LOCATION: (238789) ... (248788)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (22271)...(222816)
COTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (225381)...(224080)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
                   NAME/KEY: unsure
LOCATION: 145507
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 151967
OTHER INFORMATION: unknown
NAME/KEY: misc_feature
LOCATION: (151967) ... (1542066)
OTHER INFORMATION: n = A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (186224)...(186323)
OTHER INFORMATION: n = A,T,C or G
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LOCATION: (220360)...(220459)
OTHER INFORMATION: n = A,T,C or G
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THER INFORMATION: n = A,T,C or G
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OTHER INFORMATION: exon 1C
NAME/KEY: exon:intron junction
LOCATION: (151129)...(151130)
OTHER INFORMATION: exon 5:intron
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LOCATION: (299248)...(299249)
OTHER INFORMATION: exon 9:intron
n = A,T,C or G
                                                                                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: 154217
OTHER INFORMATION: unknown
NAME/KEY: misc feature
LOCATION: (164037)...(164136)
OTHER INFORMATION: n = A,T,C or
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LOCATION: (174557)...(174756)
OTHER INFORMATION: n = A,T,C or
OTHER INFORMATION:
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Sequence 11, Application US/10027983

Sequence 11, Application US/10027983

Patent No. 6617162

GENERAL INFORMATION:

APPLICANT: Mark P. Roach

APPLICANT: Mark P. Roach

TILLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION

CURRENT APPLICATION NUMBER: US/10/027,983

CURRENT FILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 98

SEQ ID NO 11

LENGTH: 392000
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9862 CTGGGCTCACTGCAACCTCTGCCACCCAGGTTCAAGCAATTTTCCTGTGTCAGGCTCCCA 9921
                                                                                  1565 AGTAGCTGGGACTACAGGCACTTCCCACCATGCCCAGCTGATTTTTGTATTTTTAGTAGA 1624
                                                                                                                     1625 GATGGGATTTCACTTTGTTGGCCAAGCTGGTCTTTTTGCTGTCATAATTGTTGT 1684
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LOCATION: 137740
CTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 137742
OTHER INFORMATION: unknown
NAME/KEY: misc feature
LOCATION: (138122)...(138221)
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                                                                                                                     Gaps
                                                                                             Length 392000;
                                                                                                                     43;
                                                                                           Query Match 8.2%; Score 319.8; DB 4; Length Best Local Similarity 67.2%; Pred. No. 1.1e-68; Matches 533; Conservative 0; Mismatches 217; Indels
NAME/KEY: intron
LOCATION: (348579)...(381838)
OTHER INFORMATION: intron 10
NAME/KEY: intron:exon junction
LOCATION: (386185)...(386186)
OTHER INFORMATION: intron 11:exon 12
US-10-027-983-11
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Sequence 3, Application US/09813817 Patent No. 6340583

RESULT 6 US-09-813-817-3/C

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11749 AGAATTGCTTAAACCCGGGAGGCAGAAGTTGCAGTGAGCCGAAATTGTGCCACTGCACTC 11690
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GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOU178
CURRENT APPLICATION NUMBER: US/09/813,817
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASELSEQ for Windows Version 4.0
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Pred. No. 2.6e-68;
0; Mismatches 264; Indels
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Best Local Similarity 66.7%;
Matches 561; Conservative
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; ORGANISM: Human
US-09-813-817-3
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                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09804471A

Patent No. 6479269
GENERAL INFORMATION:
FALSE INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01164
CURRENT APPLICATION NUMBER: US/09/804,471A
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                  AGGAGTICAAAACCAGCCTGGCCAACATGGTGAAAACCCCCGTCTTACTAAAAATACAAAA 1988
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                                          1441 TITITITITITITITIGAGAGAGICTIGCICTITCACCCIGGCIGGAGGGCAGIGGIG
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                                                                                                                 <u> AGAATTTCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGATCACACCACTGCACTC</u>
                                                                                                                                                                                                                                                Query Match
8.0%; Score 312.4; DB 4; Length 174493;
Best Local Similarity 61.7%; Pred. No. 5.2e-67;
Matches 490; Conservative 0; Mismatches 298; Indels 6;
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NAME/KEY: misc_feature
LOCATION: (1)...(174493)
OTHER INFORMATION: n = A,T,C or G
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US-09-804-471A-3
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001178DIV

CURRENT APPLICATION NUMBER: US/09/978,197

CURRENT APPLICATION NUMBER: 09/813,817

PRIOR FILING DATE: 2001-03-22

NUMBER: OF SEQ ID NOS: 4

SEQ ID NOS: 4

SEQ ID NO 3

LENGTH: 59065
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12226 cagecacaceceaceaceaceaecraecraerririrerarririaeraecraeceaerreaec 12167
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Pred. No. 2.6e-68;
0; Mismatches 264;
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Patent No. 6403353
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Best Local Similarity 66.7%;
Matches 561; Conservative
                                                                                               11629 A 11629
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APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOSTWARE: PATENT.
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TAGAGATGGGATTTCACTTTGTTGGCCAAGCTGGTCTCAAACTTTTTGCTGTCATAATTG 1680
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                                                                                   CTGAGGTCAGGAGTTCAAAACCAGCCTGGCCAACATGGTGAAACCCCGGTCTATAAAA
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NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 5-124-273 : polymorphic
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Patent No. 6399373
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NAME/KEY: allele
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APPLICANT: WEBSTER, Marion et al
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID WOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPREMENCE: CLOOLA64DIV
CURRENT APPLICATION NUMBER: US/10/238, 709
CURRENT PILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Fastesof for Windows Version 4.0
SEQ ID NO 3
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LCCATION: (1)...(174493)

OTHER INFORMATION: n = A,T,C or G

US-10-238-709-3
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Patent No. 6680188
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ORGANISM: Human
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COCATION: 146345
DIHER INFORMATION: 5-143-101 : polymorphic base A
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                                                                                                               LOCATION: 93714
OTHER INFORMATION: 5-128-60 : polymorphic base de FEATURE:
NAME/KEY: allele
LOCATION: 97122
OTHER INFORMATION: 99-1442-224 : polymorphic base FEATURE:
NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base OTHER INFORMATION: 5-129-144 : polymorphic base d
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LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base
FEATURE:
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NAME/KEY: allele
COATION: 99098
OTHER INFORMATION: 5-130-257:
FEATURE:
NAME/KEY: allele
LOCATION: 99117
OTHER INFORMATION: 5-130-276:
                                              NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 99-1437-325
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OCATION: 108471
VIHER INFORMATION: 5-136-174
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LOCATION: 134134
OTHER INFORMATION: 5-140-120
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AAME/KEY: allele
LOCATION: 103806
FEATURE: INFORMATION: 5-131-395
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OCATION: 108149
THER INFORMATION: 5-135-198
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NAME/KEY: allele
LOCATION: 108308
DIHER INFORMATION: 5-135-357
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THER INFORMATION: 5-140-348
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OCATION: 108106
OTHER INFORMATION: 5-135-155
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OCATION: 106940
WHER INFORMATION: 5-133-375
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NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84
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NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION: 5
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NAME/KEY: allele
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FEATURE:
NAME/KEY: allele
LOCATION: 90819...90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
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LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
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OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
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LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
SEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymoxphic fragment 5-127-261 SEQ ID52
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NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
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LOCATION: 72711..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
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LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
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LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
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LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
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NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
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DTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
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LOCATION: 72771...72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
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COCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
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NAME/KRZ: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
or
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OTHER INFORMATION: 5-145-24 : polymorphic base
                                        NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352
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NAME/KEY: allele
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NAME/KEY: allele
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10142 --AGACGGGGTTTCACCATGTTGGCCAGGCTGGTTTCAAGTAATCCACCCTCCTCAGCCT 10199
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                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: LI, JISJIN et al
APPLICANT: LI, JISJIN et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPRENCE: CL000851
CURRENT APPLICATION NUMBER: US/09/735,934A
CURRENT PILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 3
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                                     86253 TAGCCAGGCATGGTGGCGGTGCCTGTAATCCCAGCTACTCTGGAGGCTGAGGCAGGAGA
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1992 TAGCTAAGTGTGGTGGCGATGCCTGTAATCCCAGCTACTTGGGAGGGTGAGGCAGGAGA
                                                                                       2052 ATTICITGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGATCACACCACTGCACTCCAG
                                                                                                                                1442 TITITITITITITITIGAGAAGGECTIGCICTITICACCCIGGCIGGAGGGCAGTGGIGT
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Patent No. 6372468
                                                                                                                                                                                                                                                                                                                      86073 TGGCACTTAAAGA 86061
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US-09-735-934A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.9%; Score 308.2; DB 4; Length 162450; Best Local Similarity 66.7%; Pred. No. 5.6e-66; Matches 529; Conservative 0; Mismatches 233; Indels 31; Gaps
                                                                                                                                              ID37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID39
           NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
                                                                                                                                                                                                                                                                                                                             SEC ID38
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                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
LOCATION: 108084...108130
LOCHER INFORMATION: polymorphic fragment 5-135-155
PEATURE:
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LOCATION: 108127...108177
OTHER INFORMATION: polymorphic fragment 5-135-198
FEATURE:
                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155
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OTHER INFORMATION: polymorphic fragment 5-135-198
FEATURE:
                                                                                              NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375
                                                                                                                                                                                                                   LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375
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Oy 1862 GGCGTGGTGGC Db 10380 GGCACGGTGGC Oy 1922 TGAGGTCACGA Db 10438 TGAGGTCAGGA OY 1982 TACAAAAANT Db 10498 TACAAAAAATT	Oy 2042 AGGCAGGAGAA 	RESULT 13 US-09-851-886-3/C US-09-851-886-3/C Sequence 3, Application Fatent No. 6410325 GENERAL INFORMATION: APPLICANT: C. Frank Be APPLICANT: C. Frank Be TITLE OF INVENTION: APPLICANT: Andrew T. TITLE OF INVENTION: AP FILE REFREENCE: RTS-02 CURRENT APLICATION NU CURRENT APPLICATION NU CURRENT APPLICATION NU CURRENT APPLICATION NU SEQ ID NOS: TENGTH. 10000		Oy 1441 TITITITITITIT Db 50400 TIGITITIGITI OY 1501 TGATCTCAGCT Db 50340 TGATCTCAGCT OY 1561 CCCAAGTAGCT Db 50280 CCAAGTAGCT	Oy 1620 GTAGAGATGGG
Qy 1922 TGAGGTCAGGAGTTCAAAACCAGCCTGGCCAACATGGTGAAACCCGGTCTTACTAAAA 1981 Db 10438 TGAGGTCAGGACTTAGAGGCCAACATGGTGAAACCCTGTCTTCTACTACTAAAAC 10497 Qy 1982 TACAAAAATTAGTGGTGGCCATGCCTGTAATCCCAGCTACTTGGAGGGTG 2041 Db 10498 TAGAAA-AATTACTTGAACCGGGGGGGCGCATACTATAATCCCACTACTCGGGAGGCTG 10556 Qy 2042 AGGCAGGAGAATTTCTTGAACCCG-GGAGGCAGGTGCAGGGGGTGCAGGCCCCACTACTCGGGAGGCTG 100 Db 10557 AGGCAGGAGAATCATTGAACCTGAGGGGGGGGGGGGGGG	QY 2101 CTGCACTCCAGCCTGGGGGAGAGAGAGAGACTTCCTCTCAAAAAACAAAAGA 2160 Db 10617 TTGCACTCCGGCTGGGTGACAGCTCCGTCTCAAAAAAAAA	REGULT 12 VG-10-060-332-3 VG-10-060-332-3 Sequence 3, Application US/10060332 Patent No. 6528294 CHARRAL INFORMATION 1 TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: 2002-02-01 NUMBER OF SEQ ID NOS: 4 SOCTREAT FILING DATE: 2002-02-01 NUMBER OF SEQ ID NOS: 4 SEQ ID NO 3 LENCTH: 43950 TYPE: DNA CORRANISM: Homo sapiens US-10-060-332-3	7.9%; Score 307.6; DB 4; Length 43950; L; Conservative 0; Mismatches 229; Indels 6; Gaps TITITITITITITIONGARAAGAGICTIGCTCTTICACCCTGGCTGGAGGGCAGTGT [1502 GATCTCAGCTCACTCCAGACTTTCGCCTCCGGGGTTCAGCAATTCTCCTGCTTCAGCCTC 10022 GATCTCAGCTCACTCCTCCTCTCTCTTCTTTTTTTTTTT	OY 1682 TGTAACTATTGTTGCTGAGGTAGGGCCCCCAGACCAAAAATAAAT

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ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPEND)
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DD S0106GCATTGGTTACCTTTATGGTTGGCACTGGATGGATGGATGGCCATTA 50058		2100 ACTGCACCCGGGGGA-GAGAGGGAAACTCCTCTCAAAAAAAAAA	Patent No. 655351 GENERAL INFORMATION: APPLICANT: BEASLEY, Ellen M. et al APPLICANT: BEASLEY, Ellen M. et al TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CL001213 CURRENT APPLICATION NUMBER: US/09/820,924 CURRENT FILING DATE: 2001-03-30	SEQ ID NOS: 4 FastSEQ for Windows Version 4.0 39982 Human 7.8%; Score 304; DB 4; Length 39982; Similarity 56.3%; Pred. No. 3e-65;	829; Conservative 735 TATTTTTTTTTTGAAACA 734 TATTATTTTTTTGAGATG 795 TAATAGCTCACTGCAGCCT 795 TAATAGCTCACTGCAGCCT 797 TAATAGCTCACTGCAGCCT 797 TAATAGCTCACTGCAGCCT 797 TAATAGCTCACTGCAGCCT	854 GAGTAGCTGGGCTTGTGCCCCCGGCTGGCTAGTTTTAAAAATGTTTTTTTT

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GENERAL INFORMATION:
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TITLE OF INVENTION:
ACID.MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION:
TITLE OF INVENTION:
GENERAL APPLICATION NUMBER: US/09/735,934A
CURRENT FILING DAPE:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO3:
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68.2%; Pred. No. 5.6e-65;
ive 0; Mismatches 200; Indels
                                  31309 AAAAAAAAAAAAAAAAAAAAGGAACCAACTA 31278
2142 AAAAACAAAAACAAAAGAATTAAGCAAATTA 2173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 68.23
Matches 492; Conservative
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Sequence 15, Appl
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Sequence 24494, A
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Sequence 11, Appl
Sequence 1, Appl
Sequence 1569, Ap
Sequence 1584, Ap
Sequence 1584, Ap
Sequence 1584, Ap
Sequence 10, Appl
Sequence 7810, Appl
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7909.918 Million cell updates/sec
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2: /cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*
3: /cgn2 6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
4: /cgn2 6/ptodata/1/pubpna/USO6 PUBCOMB.seq:*
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7: /cgn2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
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Sequence 34, Appl	Semience 1 Appli		sequence 322, App	INFO	31, Ap	1618,		2429,	2069,	Sequence 115030,		Sequence 115030,	1150	-			3049,	Sequence 3244, Ap	2246,	904,	2429,	2069,	12	844,	7,		1945	e 194	943,	Sequence 1943, Ap
US-10-235-192A-34	10-050-141	T-TC-CT-CT-CC	-10-087-192-32	US-10-012-697-1406	US-10-235-192A-31	US-10-087-192-1618	US-10-087-192-1168	US-10-017-161-2429	US		US-10-027-632-1	SD		US-10-087-192-24	US-09-764-877-3049	US-09-764-877-3244					US-10-017-161-2429		US-09-997-722-154		US-10-01	US-09-764-869-1945	US	US-10-227-577-1945	09-764-869-19	US-10-091-504-1943
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3910; Conservative C; Mismatches 0; Indels 0;
                               Sequence 15, Application US/10016725

Publication No. US20020151018A1

GENERAL INFORMATION:

APPLICANT: Prouty, Stephen

APPLICANT: Stemn, Kurt

TITLE OF INVENTION: Stearyl-CoA Desaturase Promoter

TITLE OF INVENTION: Stearyl-CoA Desaturase Promoter

FILE REFERENCE: Vac2065

CURRENT APPLICATION NUMBER: US/10/016,725

CURRENT FILING DATE: 2002-06-10

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin version 3.1

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US-10-016-725-15
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QY 3481 GCTCCCGACGCGGGATGCCGGGCACGCGCGCGCGCGCGCG	RESULT 2 US-10-087-192-10 is Sequence 10, Application US/10087192 sequence 10, Application US/10087192 sequence 10, Application US/10087192 publication No. US20020182586A1 GENERAL INFORMATION: TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER TITLE OF INVENTION: CANCER TITLE OF INVENTION: CANCER TITLE OF INVENTION: CANCER TITLE OF INVENTION: CANCER TITLE OF INVENTION: CANCER CURRENT APPLICATION NUMBER: US/10/087,192 CURRENT FILING DATE: 2000-12-22 PRIOR PELLOR DATE: 2000-10-22 PRIOR PELLOR OF THE 2001-03-02 PRIOR PELLOR OF THE 2001-03-02 NUMBER OF SEQ ID NO 10 LENGTH: 37698 TYPE: DNA CORGANISM: Homo sapiens US-10-087-192-10 Query Match Query Match	Similarity 99.9%; Pred. 5; Conservative 0; Mi GAATTCATCCATTTAAATCATACAA GAATTCATCCATTTAAATCATACAA CATCACACATTTTAGAACAGT
2401 AGTCTACCTCCAGGAAATCCCAGGTGCTTGTCTTCCTGGGAAGTGAATCATTGGCGCAG 2460 2401 AGTCTACCTCCCAGGAAATCCCAGGTGCTTGTCTTCCTGGGAAGTGAATCATTGGCGCAG 2460 2461 CACTCCGTATTTTCCCCTCTTCCCAGGGAAGGAATTTGGGAAAAAAA 2520 2461 CACTCCGTATTTTTCTCCTTTCCCAGGGAAAGAATCCTAGGGCAGTATTTGGGAAAAAAA 2520 2521 TGGGCATGGAAGGACCCGGGGGAAAGAATCCTAGGGAAAAAAA 2580 2521 TGGGCATGGAAGGACCCGGGTGAATGCATGCTTCTGAGTTCTTGAGAAAAAAA 2580 2521 TGGGCATGGAAGGACCCGGGTGAATGCATAGCTTGCTGGTTAA 2580 2581 GGCTCCTACAGAACACGGGAAAAGATGCATAGCTTCTGAGTTCTCATGGTAA 2580 2581 GGCTCCTACAGAACACGGGAAAAGATGCATAGCCTGCTTCTGAGCTCCAGGCATC 2640 2641 TCAGGGACCGGGAAAAGATGGGACAGGGAACAAAAAAAAA	2881 AATACCTGCCAGCTATTCTTATTCCACATCCAAGCCCTTTCGCCTGCTGCTGCTGAAAA 2940 2941 AATACCTGCCAGCTATTCTTATTCCACATCCAAGCCTTTCGCCTGCTGCTGCTGGTGAAAA 2940 2941 CACATGTCAGTGTTTCCTGACGTTTCCACAAGAAGAATTCCAAAATTACAACCTGCCAG 3000 3001 TCTGAAGAATCTCCAAAACATCCCACACACACACACACAC	TCCCGCGTCCCCAAGCTCCAGATCCTGGGGTGCTGCCACGTCTCCCTGCCACGCGCCTG GGGGGACGGGAAGACGGAAGATGTTAGTGGTGGGGCGCCCCCGAGGGTTCACCACT GTTTCCTGAGAAGACGGAACGGA

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Sequence 24494, Application US/10027632

Sequence 24494, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE OF INVENTION: POLYMorphisms in the Human Genome
FILE OF INVENTION: 108027.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-00-12

PRIOR PELING DATE: 2000-00-12

PRIOR PELING DATE: 2000-00-329

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PRIOR PELING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

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1027 ö ô Query Match
16.1%; Score 630.6; DB 13; Length 631;
Best Local Similarity 99.8%; Pred. No. 2.1e-158;
Matches 630; Conservative 1; Mismatches 0; Indels 0;

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; ORGANISM: Human
US-10-027-632-24494
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GENERAL INFORMATION:
GENERAL INFORMATION:
INFORMATION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108927.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2000-04-30
PRIOR PELLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/198,676
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PRIOR APPLICATION NUMBER: US 60/199,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1000-03-29
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PRIOR FILING DATE: 1999-01-28
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'Sequence 24494, Application US/10027632

; Publication No. US20030204075A9
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SGUENCE 814, Application US/10087192

Publication No. US20020182586A1

GENERAL INFORMATION:

APPLICANT: MORIS.

TITLE OF INVENTION: CANCER

TITLE OF INVENTION: CANCER

TITLE OF INVENTION: CANCER

TITLE OF INVENTION: UNMER: US/10/087,192

CURRENT APPLICATION NUMBER: US/147,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 2059

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 814

LENGTH: 59725

TYPE: DNA
                                               Indels
  DB 16;
Query Match
16.1%; Score 630.6; DB 16
Best Local Similarity 99.8%; Pred. No. 2.1e-158;
Matches 630; Conservative 1; Mismatches 0;
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Sequence 1, Application US/09792468B; Publication No. US20030157552A1 GENERAL INFORMATION: APPLICANT: Hayden, Michael R.
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US-09-792-468B-1
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                                                                       Length 59725;
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                                                                     11.8%; Score 460; DB 13;
58.9%; Pred. No. 3.1e-111;
iive 0; Mismatches 660;
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       FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(59725)
GTHER INFORMATION: n = A,T,C or
US-10-087-192-814
                                                                               Best Local Similarity 58.9
Matches 1107; Conservative
ORGANISM: Homo sapiens
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CURRENT FILING DATE:
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NAME/KEY: CDS
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APPLICANT: Brownlie, Alison J.
APPLICANT: Ntambi, James M.
APPLICANT: Myazaki, Makoto
APPLICANT: Myazaki, Makoto
APPLICANT: Myazaki, Makoto
APPLICANT: Gray-Keller, Mark P.
APPLICANT: Attie, Alan D.
TITLE OF INVENTION: to Identify Triglyceride Reducing Therapeutic Agents
TITLE OF INVENTION: Lo Identify Triglyceride Reducing Therapeutic Agents
FILE REFERENCE: 760050-7
CURRENT APPLICATION NUMBER: US/09/792,468B
CURRENT FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 617
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APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAWA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVERTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
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Pred. No. 5.3e-110;
0; Mismatches 1;
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Best Local Similarity 99.8%;
Matches 451; Conservative (
                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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US-10-017-161-1569
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LOCATION: (9233)...[9332);
OTHER INFORMATION: a, t, c, g, unknown or other US-10-017-161-1569
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PRIOR APPLICATION NUMBER: JP 2
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1569
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FEATURE:
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NAME/KEY: CDS
LOCATION: (4089)..(4448)
NAME/KEY: CDS
LOCATION: (9336)..(9431)
FEATURE:
REATURE:
LOCATION: (3602)..(3701)
OTHER INFORMATION: a, t, c,
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NAME/KEY: source
LOCATION: (1)..(9631)
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                                                                                            CCTGAGGTCAGGAGTTCAAAACCAGCCTGGCCAACATGGTGAAAACCCCGTCTCTACTAAA
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APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Scherf, Unc C.
APPLICANT: Scherf, Uwe
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
FRIOR APPLICATION NUMBER: PGT/US01/09847
PRIOR APPLICATION NUMBER: US 60/193,446
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1584
LENGTH: 36296
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US-10-240-425-1584
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Pred. No. 8.4e-83;
0; Mismatches 609;
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Publication No. US20040033502A1
GENURAL INFORMATION:
APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
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Best Local Similarity 57.2%;
Matches 956; Conservative
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NANB/KEY: CDS	Query Match 8.9%; Score 349.8; DB 16; Length 12394; Best Local Similarity 55.2%; Pred; No. 4.3e-82; Matches 1016; Conservative 0; Mismatches 742; Indels 81; Gaps 14; Qy 370 TATTATTAGAGACGTTCTCACTCGTCACGCTGGAGTGCAGTGCACTCATCATA 429 Db 3604 TITTTTTGAGATGCACTCACTCTGCACGCTGGAGTGCAGTCAGCTCTGGAGTGATGTTTTTTTT	0y 550 AIGTATTCATTTTTTTTTTTTTTTTTABAGTTCTTAAACGCTCTCAACTTTTTTTTTT
QY 1631 ATTTCACTTTGTTGGCCAAGCTGGTCTCAAAC	Oy 1960 GAAACCCGGTCTACTAAAATACAAAAATTAGCTAAGTGGGGGGATGCCTGTA 2019	REBULT 11 US-10-181-875-10 US-10-181-875-10 Sequence 10. Application US/10181875 Sequence 10. Application US/2030216333A1 GENERAL INFORMATION: SEQUENCE 10. Monia APPLICANT: Bais Pharmaceuticals, Inc. APPLICANT: Madeline M. Butler APPLICANT: Madeline Wyatt TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXPRESSIFILE REPERRACE: RTS-0356 CURRENT TELING DATE: 2002-07-22 PRIOR APPLICATION NUMBER: 09/488,856 FILE REPERRACE: RTS-036 CURRENT APPLICATION NUMBER: 09/488,856 FILE PRIOR FILING DATE: 2000-01-21 NUMBER OF SEQ ID NOS: 88 LENGTH: 12394 TYPE: DNA ORGANISM: Homo mapiens FEATURE: NAME/KEY: CDS LOCATION: (115)(397) FEATURE: NAME/KEY: CDS LOCATION: (2438)(2625) FEATURE: NAME/KEY: CDS LOCATION: (5639)(5722)

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TYPE: DNA
CRGANISM: Homo sapiens
US-09-764-891-7810
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US-09-764-891-7810
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LENGTH: 13216
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                          4255 CTGCAACCTCTGCCTCCTGGGTTCAAGCGCTGCAACCTCTGCCTCCTGGGTTCAAGCAAT 4314
                                                       1080 ATGAATAATACTCCAGTGAATATTCATGTATTACATTTGTGTGGGCATATGTTTTCATTTC 1139
                                                                                  4315 TCTTGTACCTCATCCACCTGAGTAGTTGGAATCACAGGCGTGCGCCATGCCCAGCTA 4374
                                                                                                              TGTTGGGTTTATATCTAGGAGTGGAATTGCTGGATCCCGGGTAATATTTTGACAGGCAGA 1199
                                                                                                                                        4435 TCCTGGCCTCAAGTGATTTCCCTGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGGGGTGA 4494
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: FOOD.
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrappe NUMBER OF SEQ 1D NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
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Publication No. US20030077808A1
GENERAL INFORMATION:
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Best Local Similarity 70.0%;
Matches 516; Conservative C
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Sequence 2278, Application US/09880107; Patent No. US20020142981A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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                                    TITITITITITITITIGAGAAAGAGICITGCICTITCACCCIGGCIGGAGGCCAGIGGIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 29163;
                                                                                                                                                                                                           Sequence 7809, Application US/09764891

Publication No. US200307780BA1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

CURRENT PELLICANT: US/09/764,891

CURRENT PELLICANTION NUMBER: US/09/764,891

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

SOFTWARE: PatentIN Ver. 2.0

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 7809

LENTH: 29163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.9%; Score 347.4; DB 10; Length Best Local Similarity 69.9%; Pred. No. 3.4e-81; Matches 515; Conservative 0; Mismatches 211; Indels
                                                                                                     2161 ATTAAGCAAATTAGACA 2177
                                                                                                                                    4334 ACAAAACAAACAAAAA 4350
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-891-7809
                                                                                                                                                                                       RESULT 13
US-09-764-891-7809
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   2041 GAGGCAGGAGAATTICTIGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGATCACACCA
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                                             735 TATTTTTTTTTTCTTGAAACAGGGTATCACTCTGTTGCCCCAGGCTGGAGTACAGTGGCGTAA
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CTHER INFORMATION: Genbank Accession No. US20020142981A1 M17262 US-09-880-107-2278
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APPLICANT: Wockley, Joseph G.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENITON: Gene Expression Profiles in Liver Cancer:
TITLE OF INVENITON: Gene Expression Profiles in Liver Cancer:
TITLE OF INVENITON: Gene Expression Profiles in Liver Cancer:
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR PILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
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8.8%; Score 342.8; DB 9;
Best Local Similarity 57.5%; Pred. No. 5.5e-80;
Matches 848; Conservative 0; Mismatches 552;
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APPLICANT: McCarthy, Jeanette
TITLE OF INVENTION: Methods and Compositions for Identifying
TITLE OF INVENTION: Risk Factors for Abnormal Lipid Levels and the Diseases
TITLE OF INVENTION: and Disorders Associated Therewith
FILE REFERENCE: MMI-011
CURRENT APPLICATION NUMBER: US/10/235,192A
CURRENT FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
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Pred. No. 5.5e-80;
0; Mismatches 552;
                                                   ; Sequence 34, Application US/10235192A; Publication No. US20040043389A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.5%;
Matches 848; Conservative
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RESULT 15
US-10-235-192A-34
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              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                    ORGANISM
                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                  /note="Organ: brain, Vector: pGWV-SPORT6; Site_1: NotI; /note="Organ: brain, Vector: pGWV-SPORT6; Site_1: NotI; /note="Organ: brain, Vector: pGWV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                         2; Gaps
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Best Local Similarity 99.5%; Pred. No. 8.8e-86;
Matches 643; Conservative 0; Mismatches 1; Indels 2;
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location/Qualifiers
                                                                                                                       /lab_host="DH10B"
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B1559696 579 bp mRNA linear EST 05-SEP-2001 603252566F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5294921 5',

BISS9696 LOCUS DEFINITION

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (Dasses 1 to 579)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Preparation: Michael J. Brownstein (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Tncyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov

Llocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NIHH MGC_97"
/clone_lib="NIHH MGC_97"
/note="Organ: testis; Vector: pBluescriptk (modified pBluescriptk K8+) Site_1: BamHI, Site_2: Sall-XhoI (gtcgag); Oligo-dT primed using primer
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:5294921"
/lab host="DH108"
BI559696
BI559696.1 GI:15447010
                                                                                        Homo sapiens (human)
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Tausoner, R.D., Colling, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Zoeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Zoederg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Biatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheir, S.F., Tokhivki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Norkernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S., Worley, K.C., Hale, S., Gardia, A.M., Gay, L.J., Hulyk, S.W., Wilalon, D.K., Malek, J.A., Gunarane, P.H., Richards, S., Sanchez, A., Mitting, M., Sodergren, E.J., Lu, X., Gibbs, R.A., Faley, J., Helton, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodrigues, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodrigues, R.W., Touchman, J.W., Green, E.D., Butterfield, Y.S., Krzywinski, M.I., Salska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse odnA sequences of the sci. U.S.A., 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acussolu 2076 bp mRNA linear HTC 19-NOV-2003
Homo sapiens sialophorin (gpL115, leukosialin, CD43), mRNA (CDNA
clone IMAGE:5094058), with apparent retained intron.
EC035510
                                                                                                                                                                                                                                                                                                                                                       714 CCTTTGGGAGGCCGAGGCGGGTGGATTGCTTGAGCTCAGGAGTTCAAGATTAGCCTAGGG 655
                                                                                                                                                                                                                                                                                                   535
                                                                                                                                                                                                                                                                                                                                                                                                                  534 TGAGGCTGGAGTGAACTGTAATCCTACAACTGTACTCCAGCCTGGGCAACAACAGAT 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2076)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                   594 CACCTGTAGTCGTAGCTATTTGGGAAGCTGAGATGGGAGGATTGCTTGAGCCTAGGAGAT
                                                                                                     1952 AACATGGTGAAACCCCGTCTCTACTAAAATACAAAAATTAGCTAAGTGTGGTGGCGCA
                                                                                                                                                                                                                           2012 IGCCIGIAATCCCAGCTACTIGGGAGGGTGAGGCAGGAGAATTTCTTGAACCCGGGAGGC
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2132 TTCCTCTCAAAAAAAAAAAAAAAAAAAATTAAGCAAATTAAGAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC035510.1 GI:23271054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 2076)
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AUTHORS
TITLE
JOURNAL
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BC035510
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KEYWORDS
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PUBMED
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                      cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Web Site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,U., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 79 Row: d Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identity to protein
This clone has the following problem: retained intron.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:5582524"
/tissue_type="Tedfis, embryonal carcinoma"
/clone_lib="NIH MGC_92"
/lab_host="DH10E"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Tissue Procurement: ATCC
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Db ò 셤 à 셤 ð g à g à qq ò 셤 ઠે 셤 Ŋ

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2020 ATCCCAGCTACTTGGGAGGGTGAGGCAGGAGTTTCTTGAACCCGGGAGGCAGAGGTTG 2079
                                                                                                                                                   2080 CAGTGAAGCGAGATCACACCACTGCACTCCAGCCTGGGGGAGAGAGCGAGACTTCCTCTC 2139
                                                                                                                                                                                                                  1373 chdridagccdadarchcccchridchcricchdccridgcchachagaaacriccarcr 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC038630 2772 bp mRNA linear HTC 04-MAR-2003
HOMO sapiens, Similar to hypothetical protein FLJ20489, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-CCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 73 Row: i Column: 4 This clone has the following problem: retained intron. Location/Qualifiers
                                                                                1313 Arcccascracrissassascrassassas arccrisaacccassassassas
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/clone_lib="NHM MGC 95"
/lab_host="DH108"
/note="Vector: pBluescript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 189;
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69.5%; Pred. No. 2.4e-35;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5263792"
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                                                                                                                                                                                                                                                                                                                                                    1433 CAAAAAAAAAAAAAAGGAGATA 1453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMAGE:5263792, mRNA.
BC038630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskelllo,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAL Plate: 39 Row: p Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
This clone has the following problem: retained intron.

I. 2076

//crganiam=Homo sapiens"
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al Similarity 67.2%; Pred. No. 2.9e-35;
498; Conservative 0; Mismatches 214; Indels
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/db_xref="taxon:9606"
/clone="lYAAGE:5094058"
/tissue_type="Lymph, Burkitt lymphoma"
/clone_lib="NIH MGC 8"
/lab_host="DH10B-R"
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COMMENT
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                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 73 Row: i Column: 4
This clone has the following problem: retained intron.
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Anup Madan, Jessica Fahey, Brin Helton, Mark Ketteman, Anura
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                             Length 2772;
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                                                                                                                                                                                                                                                                                                                                                                                   7.2%; Score 283.4; DB 11; Length ilarity 66.1%; Pred. No. 3.1e-34; Conservative 0; Mismatches 216; Indels
                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:5263792"
/clone="issue type="Brain, hippocampus"
/clone="lib="NIH_MGC_95"
/lab_hst="DH108"
                                                                                                                                                                                                                                                                                                                               'note="Vector: pBluescript"
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L (Dazes I to 2016)

Strausberg, L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, M.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haieh, K.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Yillalon, D.K., Mazny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and intital analysis of more than 15,000 full-length
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Contact: MGC help desk

Email: cgapba-rafmail.inl.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing Dy: National Institutes of Health Intramural

Sequencing Center (NISC),

Maryland;

Web site: http://www.nisc.nih.gov/

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc.mgc@nhgri.nih.gov/

Contact: nisc.mgc@nhgri.nih.gov/

Contact: N. Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakealey, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Legaspi, R.,

Mautro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H. and Green, E.D.
                                                         HTC 19-NOV-2003
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                                                BC035510

2076 bp mRNA linear HTC 19-NOV-20 HOMO sapiens sialophorin (gpL115, leukosialin, CD43), mRNA (cDNA clone IMAGE:5094058), with apparent retained intron.
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                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 2076)
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Direct Submission
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AUTHORS
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Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 39 Row: p Column: 13 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not

identity to protein This clone has the following problem: retained intron.

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mRNA
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Matches 462;
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                                                                                                                                                                                Query Match 7.0%; Score 273.4; DB 11; Length 2076; Best Local Similarity 67.4%; Pred. No. 1.3e-32; Matches 487; Conservative 0; Mismatches 206; Indels 30;
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                                             /mol_type="mRNA"
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   location/Qualifiers
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BU175345 AGENCOURT_7936105 NIH_MGC_92 Homo sapiens CDNA clone IMAGE:6011997

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/usutamis now, saptems
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/db_cref="taxon:9606"
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/clone_lib="NHH MGC 92"
/clone_ib="NHH MGC 92"
/note="forgan: testis, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1, Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 749)
Mart-MOC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLMM13202 row: i column: 22
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Location/Qualifiers
1. 749
BU175345.1 GI:22689329
                                                                                                                           Homo sapiens (human)
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450 GCCTGGTGGCTCATGCCTGTAATTCTGGCAGGCCAAGGCAGGC	BC035771 Homo sapiens RAD1 homolog (S. pombe), mRNA linear HTC 19-NOV-2003 IMAGE:5582524), with apparent retained intron. BC035771 BC035771. GI:23958889 HTC. HTC.	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 1910)	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Binerow, W., Shenmen, C.M., Schuler, G.D.,	Hopkins, R.F., Jordan, H., Moure, T., Max, S.I., Wang, J., Heieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubing, G.M., Hong, L., Stanleton, M. Bonsldo, M. B. Bonsldo, M. B. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M. Snares, M. B. Bonsldo, M. F. Stanleton, M	Scheetz, T. E., Brownstein, W. J., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,	AGYZAMSON,K.D., Muliahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,	Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helron, E., Ketteman, M., Madan, A., Rodrigues, S.,	Sanchez, A., Whiting M., Madan, A., Young, A.C., Shevchenko, Y., Blukfard, G.G., Blakeelley, R.W., Touchman, J.W., Green, E.D., Dickson M. C. Rodrinner & C. Crimina, G. Reen, E.D.,	Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, T.F., Tones, C., and Marce, M., M. Schein, T.F., Tones, C., and Marce, M., M. Schein, T.F., Tones, C., and Marce, M., M. Schein, T.F., Tones, C., and Marce, M., M. Schein, T.F., Tones, C., and Marce, M., M. Schein, T.F., Tones, C., and Marce, M. Smailus, D.E.,	Generation and initial analysis of more than 15,000 full-length human and mouse chNa semisones	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 22388257	12477932 12477932 12 (bases 1 to 1910) Straicher P		ancer Genomics Office, National ve, Room 11A03, Bethesda, MD 20	USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact. MGC bols 2001	Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC	CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNE)	DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),	<pre>Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/</pre>	Contact: nisc_mgc@nhgri.nih.gov
8 6 6 6 6 6 6 6	RESULT 11 BC035771 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	E E	AUTHORS							TITLE	JOURNAL	PUBMED REFERENCE ATTHORS	TITLE		REMARK					

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 79 Row: d Column: 15
This clone was Balected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
This clone has the following problem: retained intron.
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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gugan, J., Hagnighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C. McDowell, J., Pearson, R., Stantripp, S., Thomas, P.J., Touchman, J.W. Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              687 CAATCCACCCCCCCCCCCCAAAGGCTGGGATTACAGGCGTGAGCTATCATGCCTG
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64.8%; Pred. No. 5.4e-32;
Live 0; Mismatches 236; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/db_xref="taxon:9606"
/db_me="ImAGE:5582524"
/tissue_type="Testis, embryonal carcinoma"
/clone_lib="NIH MGC_92"
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Best Local S:
Matches 471
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2039 GTGAGGCAGGAGAATTTCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGATCACAC 2098

OY 1621 TAGAGATGGGATTTCACTTTGTTGGCCAAGCTGGTCTCAAACTTTTTGCTGTCATAATTG 1680	1801 CTCAGGAGTAGAGGTGATCTCTGCTCGAAAGAATAGAAT		RESULT 13 BU616025 LOCUS BU616025 BU616025 BU616025 BU616025 BU616025 BU616025 BU616025 BU616025 ACCESSION BU616025 VERSION BU616025 Homo sapiens cDNA clone CRYPTORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ADM Sapiens Buf16025.1 GI:23282240 CRGANISM Homo sapiens Bu616025 Homo sapiens Bu616026 Homo sapiens Bu616026 AMM REAZOA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; AMM AMM Alla; Eutheria; Primates; Catarrhini; Hominidae; Homo.	MATHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. TITLE Tumor Gene Index TUMOr Gene Index TOTALI Index Gene Index JOURNAL TOTALISHER (1997) CONTEST: Robert Strausberg, Ph.D. Email: cgapbe-r@mail.nih.gov Tissue Procurement: Dr. Jose Mercuende CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CLONA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CLONA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CLONA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CLONA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CLONA Dr. M. Bento Soares, bento-soares du The following repetitive elements were found in this cDNA sequence: 9-305, >ALU (matched compliment) 326-387, >LIMB7#LINE/LI
	RESULT 12 AL580585 LOCUS LOCUS AL580585 AL580585 AL580585 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-JUN-2003 BETINITION AL580585 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED ACCESSION WERSION AL580585 AL580585 GI:31318853 KEYWORDS SOURCE Homo sapiens (human) CORGANISM Homo sapiens (human) BUKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; EUARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D. TITLE AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D. TITLE COMMENT On Feb 16, 2001 this sequence version replaced qi:12346748.	National de Sequencage sedex - France scope.cns.fr, Web : www.genos icted by Life Technologies, aquence belongs to sequence ocut this cluster, see ocut this cluster, see filiang@lifetech.com URL : cryitrogen.com/ InvitroGen Co hualifiers ""RMAM" ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE ""TECHNOSE SEQUENCE "TECHNOSE SEQUENC	b_xref="ta lone="CS0" lone="CS0" ell_line=" lone line=" lone line" cte="lst s iner Five gested wit; tes of the	Similarity 62.2%; Pred. No. 2.9e-30; 7; Conservative 14; Mismatches 245; Indels TITITITITITITITIAGAAAGGTTTTTGCTCTTTCCCTGGCTGGTTGCTTGCTTG

GSS 06-NOV-2000

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2038 GGTGAGGCAGGAGAATTTCTTGAACCCGGGAGGCAGGGTTGCAGTGAAGCGAGATCACA 2097
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                                                                                                                  1442 TITITITITITITITGAGAAAGAGICTTGCTCTTTCACCCTGGCTGGAGGGCAGTGGTGT 1501
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Medicine and Radiology
Duke University Medical Center
Box 2610, MSRB, Room 117, Durham, NC 27710, USA
part of a 1.4 megabase_contig including the LOH11A metastasis
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6.5%; Score 255.8; DB 28; Length 2971;
Best Local Similarity 65.4%; Pred. No. 5.1e-30;
Matches 478; Conservative 0; Mismatches 177; Indels 76;
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/map="11p15.5"
/clone="pTMB59.14"
/clone_lib="Human"
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Pred. No. 3.7e-30;
0; Mismatches 216; Indels 38;
                                                                                                                                                                                                                                                                          /clone="UI-H-DF0.ben-m-20-0-UI"
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Seq primer: M13 FORWARD POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.6%;
Best Local Similarity 64.7%;
Matches 465; Conservative (
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S Lin, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
L Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqreféquencoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2057.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODK001AB07NP1&cluster=2057.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
Faraday Avenue Genoscope sequence ID : CSODK001AB07NP1.
                                                1861
                                                                                                                      1862 GGCGTGGTGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCATGTGGATTCACC 1921
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                                                                              ------TTTATGGTGAAAGACTGAATGTTTTCTAAGATCAGAAACAGCCA 827
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/cell line="HELA"
/cell line="HELA"
/clone lib="HGmo sapiens HELA CELLS COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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AL578531 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens CDNA clone CS0DK001YC13 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                            TCAGGAGTAGAGGTGATCTCTCGGAAAGAGAAATAGAATGAAAATATTCTCCGGGCCA
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734 AAGIGCIGGGATTACAGGCATAAGCCACCGCATCTGGCCCAACATTATAT--
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'db_xref="taxon:9606"
'clone="CS0DK001YC13"
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AL578531/c
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VERSION
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AUTHORS
TITLE
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COMMENT
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                                                                                                                                                                                                                                                                          CCCAAGTAGCTGGGACTACAGGCACTTCCCACC---ATGCCCAGCTGATTTTGTATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      704 GIGGICIGCCCACITCCGCCICCCAAGIGITGGGATTATGGCC---ATTAGCCACATGI
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                                                      Gaps
                                                      15;
           Length
                                                      Indels
    6.5%; Score 255.2; DB 9;
62.2%; Pred. No. 1.2e-29;
iive 23; Mismatches 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2155 AAAAGAATTAAGCAAATTAGACAT 2178
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Query Match
Best Local Similarity 62.2%
Matches 463; Conservative
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us-10-016-725-15_copy_1_3958.rge

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May 12, 2004, 16:32:19 ; Search time 24113.2 Seconds (without alignments) 7114.428 Million cell updates/sec
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1 aggaattcatccatttaaat.....gggacctccacgcacgcgg 3958
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                  OM nucleic - nucleic search, using sw model
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Database :

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ery tch	999.00	6.2 185644 5.5 1970 4.4 161827	6 179879	3.2 17088 2.6 617	1.6 164201 1.3 200288	0.7 190508	0.5 44496	0.3 183690	0.3 170528 0.3 217615	0.2 137289	0.2 181597	0.2 187734 0.2 204963	0.0 179599	0.0 195558 9.9 155559	9 169835	9 139632	9 171555 9 181891	8 67199	8 1/2421 8 112364	8 73162	7 140529	7 133475	7 189639	6 150681	6 187064	51400T 0
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ALIGNMENTS

linear PAT 21-NOV-2002	Vertebrata; Buteleostomi;	
AX528729 4150 bp DNA Sequence 15 from Patent W00236780.	Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Ammmalia; Butheria; Primates: Catarrhin; Hominiaas: Homo	1 Prouty,S.M., Zhang,L. and Stenn,K.S. Stearoyl-coa desaturase gene promoter Patent: WO 0236780-A 15 10-MAX-2002;
KESULT 1 LOCUS AX528729 LOCUS AX528729 DEFINITION Sequence ACCESSION AX528729	S	REFERENCE 1 AUTHORS Prout TITLE Stear JOURNAL Pater

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90 Q7	6 6 6	<i>\$</i> 6	cy Dp	OY Ob	Q7 DP	QX DP	à a	<i>∂</i> 3 6	λ Q	SP SS	δ. Dp	δλ Op	QY	Sy Dp	% 93	λo
Johnson & Johnson Consumer Companies, Inc. (US) Location/Qualifiers source 14150 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	<pre>Query Match Best Local Similarity 100.0%; Score 3958; DB 6; Length 4150; Matches 3958; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy</pre>) E			QY 241 GTGAGACTTTGTGACTGGCTTTCACTTAGCATTCTATTTAAGGCTCATTATTA 300 Db 241 GTGAGACTTTGTGACTGGCTGCTTTCACTTAGCATTCTATTTTAAGGCTCATTAGGTT 300	Qy 301 CAGTACTTAGCAGTACTTCATTTTTTATTCTCAAATGGTATTCCACTGTGTGGGTAT 360 	116GC 116GC 116GC						TGGA	SCTCAAGCAATCCGCTG 84		AAAAAATGATTTTTGGTATAGAGGAGGTCTTGCTATGTTGCTCAGGCTGTATTTTATTG 9

	Db 3181 AGAGCCATTGTTCGCAGGCGTACCGAGC QY 3241 TCCCGCGTCCCCAAGCTCCAGATCCTGC	Oy 3301 GGGGGACGGGAAGACGGGACGGACGGACGTGT	Oy 3361 GTTTCCTGAGAAACTTCCCCAGTGCCCA	Qy 3421 CCTGGGCTAGGCTCCGGGCCCCAGCCCC	Oy 3481 GCTCCCGACGCGGGATGCCGGCCACAGG	Oy 3541 AGAAA CAGAGGGAGGGGAGCGAGGG 	Oy 3601 GCCAATGGCAACGGCAGGACGAGGTGGC 	Qy 3661 GITTACAGAAGCCTCAITAGCAITTCCC	QY 3721 TGTGGTGTCGGTGTCGGCAGCATCCCCGG	Qy 3781 TCTGTCTCCTCCCCTCCGCCCTACC:	3841	Qy 3901 CACCGGTGGCAGCTCTAGATT		DEFINITION Home sapiens stearcyl-CoA desata ACCESSION AF320307 VERSION AF320307.1 GI:14150490	_	Mammalia; Eutheria; Primates; C REFERENCE 1 (bases 1 to 4150) AUTHORS Zhang, L., Ge, L., Tran, T., Stenn TITLE Isolation and characterization
1981 ATACAAAAATTAGCTAAGTGTGGTGGCGCATGCCTGTAATCCCAGCTACTTGGGAGGGT 2040 2041 GAGGCAGGAGAATTTCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGATCACACCA 2100 2041 GAGGCAGGAGAATTTCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGATCACACCA 2100 2041 GAGGCAGGAGAGATTCTTGAACCCGGGAGGCAGAGGAGATGAAGAAAAAAAA	2101 CTGCACTCCAGCCTCGGGGGGGGGGGGGGGGGGGGGGGG			2341 GGTCACTGGCCAGAGAGTTGGCCTTGACCTGAGAGCGGCCAACAAAAGGAGCTGCTT 2400 	2401 AGTCTACCTCCCAGGAAATCCCAGGTGCTTGTCTTCCTGGGAAGTGAATCATTGGCGCAG 2460 			2581 GGCTCCTACAGACACGGAAAAGATGGGGCACAGGGACAGATCAGTAGGGTCAGAGCATC 2640 	0 0	2701 GTTTCHGGGCTCAACHGCCAGCTCCGTCACTTACHGGTGGTGGTGACGATGGGCAAGTTA 2760 	2761 TICCAICICICCATAICICITICCCICACTITIAAAAIGGAATAAIGGGGAACCCACCTCC 2820 	2821 CAGGGTCACAGAGAGCCTTACAGAAACGATTCTTGTGAATTGGCTTGCAGTAATAATTC 2880 	2881 AATACCTGCCAGCTATTCTTATTCCACATCCAAGCCCTTTCGCCTGCTGGTGAAAA 2940 	2941 CACATGICAGIGITICCIGACGGITICCACAAAGAATICCAAAATTACAACCIGCCAG 3000 	3001 TCTGAAGAATCTCCAAAACATCCCGCAGGGATCCTGGAGGCGCGGCCTTGGGGATGGGAC 3060 	3061 TGCCCGCCCGGGTCCTGAACAGGATGCCGTGCGCGCACACACA
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Oy 361 CCCATATCATATTAGAGACAGGTTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGC 420 Db 361 CCCATATCATTATTAGAGACAGGTTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGC 420 Qy 421 ACAATCATAGCTCACTGTAACCTCAAACTCCTGGGCTCAAGTGATCCTACGAGCGCTGGC 480 Db 421 ACAATCATAGCTCACTGTAACCTCAAACTCCTGGGCTCAAGTGATCCTACTACCTCAGGCC 480 Qy 481 TCCAGAGTAGCTAGGACTACAGGCCAACCATACCTGGCTAATTTTTTTT				901 AAAAAA 901 TTGAG7 961 TTGAG7 961 TTGAG7 1021 TCTTA1	DD 1021	1201 TCAGGGGAAGAAAACTTGGGAAAATGAAGCATGTTTAGAAATCAGCAAGAGTGCAGGG
				3 1 3		
JOURNAL Biochem: J. 357 (Pt 1), 183-193 (2001) MEDLINE 2130646E. PUBMED 1141548 REPERENCE 2 (bases 1 to 4150) AUTHORS Direct Submission JOURNAL Submitted (09-NOV-2000) Skil Biology TRC, Johnson and Johnson, Location/Qualifiers SOURCE 1.4150 Location/Qualifiers SOURCE 1.4150 1. 4150 1. 4150	signal	TATA_signal 38693872 /gene="SCD" TATA_signal 39243927 /gene="SCD" MENA <3958>4129 /gene="SCD" /product="stearoyl-CoA desaturase" /note="3602"	exon <39584129 /gene="scD" /number=1 5'UTR 39584102 /gene="scD" CDS 4103>4129 /codom_start=1 /product==sfcDm* /codom_start=1 /product=sfrearoyl-CoA desaturase" /nrofein ia-marase10.10	/protein intro / protein into / protein into / protein intro / protein intro / protein intro / protein intro / protein intro / protein intro / protein / protein / protein / protein / protein intro / protein / protein / protein intro / pro	1958, Conservative 0 1 AGGAATTCATCCATTTAAATT 1 AGGAATTCATCCATTTAAATT 1 AGGAATTCATCCATTTTAAATT 61 ATCCATCACAATCTTTAC 61 ATCCATCACAATCTTTAC	CTAC CTAC CTAC CTAC ACAT ACAT STTA STAT

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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                       Insert size: 167000; agarose-fp
Insert size: 158251; sum-of-contigs
Quality coverage: 4.9 in Q20 bases; agarose-fp
Quality coverage: 5.2 in Q20 bases; sum-of-contigs
             Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 155177 bases at least Q40 Consensus quality: 155177 bases at least Q20 Consensus quality: 157011 bases at least Q20
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9: contig of 12378 bp in length

9: gap of 100 bp

1: contig of 20429 bp in length

1: gap of 100 bp

1: contig of 26413 bp in length

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2: contig of 30346 bp in length

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2397: gap of 100 bp
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5819: gap of 100 bp
10149: contig of 4330 bp in length
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                                                                                                                                                           3721 TGTGGTGTGTCGGCAGCATCCCCGGCGCCTGCTGCGGTCGCCGCGAGCCTCGCCC 3780
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                                                                   TGTGGTGTCGGTGTCGGCAGCATCCCCGGCGCCTTGCTGCGGTCGCCGCGAGCCTCGGCC 3780
                                                                                                                                                                                                                                                    3841 TCGCACTTTGCCCCTGCTTGGCAGCGGATAAAAGGGGGCTGAGGAAATACCGGACACGGT 3900
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3601 GCCAATGGCAACGGCAGGACGAGGTGGCACCAAATTCCCTTCGGCCAATGACGAGCCGGA 3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC018783 159351 bp DNA linear HTG 14-MAR-2000
Homo sapiens clone RP11-2M13, WORKING DRAFT SEQUENCE, 12 unordered
                                                                                                                                                                                                                                                                                                                                                                                       3901 CACCCGTTGCCAGCTCTAGCCTTTAAATTCCCGGCTCGGGGACCTCCACGCACCGGGG 3958
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159351)
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L2667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-2M13
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seg.wi.mit.edu
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HTG; HTGS PHASE1; HTGS DRAFT.
HOmo sapiens (human)
Homo sapiens
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AUTHORS
TITLE
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KEYWORDS
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JOURNAL
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Decay	OY 3902 ACCCGTTGCCAGCTCTTAAATTCCCGGCTCCGGGACCTCCACGCACCGCG 3958
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COMPARTY DEGREE SEQUENCE SEARCH STATES AND STATES SEQUENCE SEARCH STATES SEQUENCE SEARCH SEARCH STATES SEQUENCE SEARCH SE	CATATCATATTATAGAGACAGGITCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGCAC CATATCATAT	65432 CTCAGCATCCTGAGTAGGACTACAGGCTTGTGCCCCCGCCAGCTAAGTTTTAA 65491	1023 TTATCTGTTCATTAGTCAGTGACATTTAGCTTGTTTCCACTTTTTGACCATTATG 1082 [CAGGGAAGAAAACTTGGAAAATGAAGCATGTTTAGAAATCAGCAAGGGGT CAGGGGAAGAAAATTAATTTTTTTTTT
Trequests: cloneraquest@sanger.ac.uk During sequence assembly data is compare Where differences are found these are are Unity geogenere assembly data is compare Where differences are found these are are corresponding to the overlapping clone, only a small overlap as described above. This sequence was finished as follows un regions were either double stranded or schemistry or covered by high quality data 30 is an attempt was made to resolve all as compressions and repeats; all regions compressions are used to associate print in the feature table with their source symboly was confirmed by restriction di abbreviations are used to associate print in the feature table with their source symboly was confirmed by restriction di abbreviations are used to associate print in the feature table with their source symboly was confirmed by restriction di abbreviations are used to associate print http://www.sanger.ac.uk/RepChAIO chttp://www.come.ac.uk/RepChAIO chttp://www.come.ac.uk/RepChAIO chttp://www.come.ac.uk/RepChAIO chttp://www.come.ac.uk/RepChAIO chttp://www.come.ac.uk/RepChAIO chttp:/	3 4 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8	B & B & B	8 6 8 6 8	3
면 보고	clonerequest@sanger.ac.uk 2001 this sequence version replaced gi:14586033. uence assembly data is compared from overlapping clones. where as are found these are annotated as variations were corlapping clone name. Note that the annotation may not be found in the sequence submission ing to the overlapping clone, as we submit sequences with loverlap as described above. I overlap as described above. I overlap as described above. I overlap as described above. I overlap as described above. I overlap as described above. I overlap as described above. I overlap as described as follows unless otherwise noted: all receipt was made to resolve all sequenced with an alternate or covered by high quality data (i.e., phred quality >= tempt was made to resolve all sequencing problems, such sions and repeats; all regions were covered by at least das confirmed by restriction digest. The following ons are used to associate primary accession numbers given true table with their source databases: Em:, EMBL; Sw:, TERMBL; Wp:, WORMPEP; Information on the WORMPEP and be found at an be found at the snager centre Chromosome 10, constructed by the Sanger Centre Chromosome 10, constructed by the Sanger Centre Chromosome 10, sanger.ac.uk/Mgy/Chr10. 10, constructed by the Sanger Centre Chromosome 10 is from the library MCl-11.1 constructed by the group is form the library Mcl-11.1 constructed by the snager centre Chromosome 10. sanger.ac.uk/Mgy/Chr10. I finay be shorter because we sequence overlapping the of clone content overlapping ight end of clone RPI1-34D15 is at 11278 in this high true left end of clone RPI1-285F16 is at 5000 inc. The true right end of clone RPI1-285F16 is at 5000 inc. The true right end of clone RPI1-285F16 is at 5000 ince.	tion/Qualifiers 115278 anism="Homo sapiens" type="genomic DNA" xref="taxon:9606" omcsome="10" ne="RRPI1-34D15" ne="Ib="RRPCI-11.1"		

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      64479: gap of 100 bp 66479: gap of 100 bp 66477 gap of 100 bp 114355: contig of 47508 bp in length 114355: gap of 100 bp 125406: contig of 10551 bp in length 125506: gap of 100 bp 125506: gap of 100 bp 127773: gap of 100 bp 127773: gap of 100 bp 130111: contig of 2167 bp in length 130111: contig of 2187 bp in length 130211: gap of 100 bp 13254: contig of 2493 bp in length 136577: contig of 4083 bp in length 136577: contig of 4083 bp in length 136577: contig of 4083 bp in length 136577: contig of 4083 bp in length 139227; contig of 42128 bp in length 131555: contig of 42128 bp in length 18155; gap of 100 bp 18155; contig of 2069 bp in length 18524; gap of 100 bp 18524; contig of 2069 bp in length 18524; gap of 100 bp 18524; contig of 2069 bp in length 18524; gap of 100 bp
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                                                                                                                                                                                                                                                                                                                    68430 CGCACTITGCCCCTGCTTGGCAGCGGTAAAGGGGGCTGAGGAAATACGGACACGGTC 68489
                                                                                                                                                                                                                       AL391723 185644 bp DNA linear HTG 11-SEP-2001
Homo sapiens chromosome 10 clone RP11-38B21, WORKING DRAFT
SEQUENCE, 14 unordered pieces.
                                                                     TITACAGAAGCCTCATTAGCATTTCCCCAGAGGCAGGGGCAGGGGCAGGGCAGGGCGGGGGGGTGGT 68309
                                                                                                                 3781
                                                                                                                                                                                               CGCACTITGCCCCTGCTTGGCAGCGGATAAAGGGGGCTGAGGAAATACCGGACACGGTC 3901
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                     68490 ACCCGTIGCCAGCTCTAGCCTTIAAATTCCCGGCTCGGGGACCTCCACCGCGG 68546
                                                                                                                                                                                                                                                                                                                                                                  3902 ACCCGTTGCCAGCTCTAAGCCTTTAAATTCCCGGGGTCGGGGACCTCCACGCACCGCGG 3958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGGTGGGTGTCGGCAGCATCCCCGGCCCCTGCTGCGGTCGCCGCGAAGCCTCGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 175002 bases at least Q40
Consensus quality: 175002 bases at least Q30
Consensus quality: 182156 bases at least Q20
Insert size: 184344; sum-of-contigs
Insert size: 140788; 6.0% error; agarose-fp
Quality coverage: 4.15x in Q20 bases; sum-of-contigs Quality
coverage: 6.51x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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59210: gap of 100 bp
61285: contig of 2075 bp in length
61385: gap of 100 bp
64379: contig of 2994 bp in length
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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Center project name: bA38B21
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Mammalia; Eutheria; Primates;
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HTG; HTGS PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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AUTHORS
TITLE
JOURNAL
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C.M.D., Haardt,M., Goldberg,Y.P., Nwaka,S.O., J., de Antueno,R.J. and Knickle,L.C. , uses thereof, and compounds for modulating A 21 23-MAY-2002; (CA) Jalifiers "Homo sapiens" "unassigned DNA" taxon:9606" ; Score 1799.8; DB 6; Length 1970; ; Pred. No. 0;), Mismatches 2; Indels 3; Gaps	TCAAAAAAACAAAAACAAAAAATTAAGCAAATTAGACATTG 218G TCAAAAAAACAAAAAACAAAAAGAATTAAGCAAATTAGACATTG 0 GGGTCAGACCACGTACAGATTTCTGTGCCAAATTAGACATTG 224G GGGTCAGACCACGTACAGATTTCTGTGCCAAATTGAGCAAGTACT 120 GGGTCAGACCACGTACAAATTTCTGTGCCACATGCCAAGTACT 120 TGAGGTGTCCACATCTGAAATCATCCAGTCTTGTTCAGAACTT 180 CCAGGACTGGAATGCACTCTCAGTCTTGTTCAGAACTT 180 CCAGGACTGGAATGCACTCTCAGTCTTGTTCAGAACTT 180 CCAGGACTGGAATGCAGTCTCCTGGTCACTTGTTCAGAACTT 180 CCAGGACTGGAATGCAGTCTCCTGGTCACTTGTTCAGAACTT 180 CCAGGACTGGAATGCAGTCTCCTGGTCACTTGTTCAGAACTT 180 CCAGGACTGGAATGCAGTCTCCTGGTCACTCCCCAGAAGTTG 240 CCAGGAACTGAATGCAGTCTCCTGGTCACTCCCCAGAAACTC 299 TAGGGAACTGAATGCAGTCTTAGCCCAGCACACACAGAAATC 240 TTAGGGAACTGAATTTCGGCAAAACACTGGCCACAAAATTTTCTCCTCTT 359 TTAGGGAACTGAATTTTCGGAAAACACTGGCCATATTTTCTCCTCTT 359 TTAGGGAACTCTCAAGACCTCCAGAAAAA 479 CCTGGTTCTGGACTCTCAAGACCTCCAAAGACACTGGAAAAA 479 CCTGGTTCTGGACTCTCAAGACCTCCAAAGACACTGGAAAAA 479 AAAAACAACAAGACATCAGGCACTCAAAGACACTGGAAAAA 579 AAAGACCTTGGGCAAAACATCAGGCACTCAAAGACACTGGAAAAA 579 AAAGACCTTGGGCAAAACATCAGGCACTCAAAGACACTGCCA 272 TTAAGAGCTTCTGAACAAACACTCAAGACACTCCAAACACTGCCA 272 TTAAGACCTTCAAGACATCTCTAAGACTCCTAAAACACTGCCA 272 TTAAGACCTTGGGCTCTCAAAAGACTCTCCAAACTGGGCAAAATT 539 AAAAACAACAACAAGACATCTCTAAGACACTCCCAAACTGGCAAAATT 539 AAAAACAACAACAAGACATCTCTAAGACTCCAAACTGGCAAAATTTCTGGGCAAATTTTCTGGGCTCCAAACTGGCCAAACTTCTCTAAACTGGCCTCCAAACTGGGCAAAATTTTCTGGGCAAAATTTTCTGGGCTCCAAACTGGCCAAACTTCTCCAAACTGGCCAAAATTTTCTGGGCTCCAAACTGGCCAAACTTCTCTCCAAACTGGCCAAACTTCTCTCCAAACTGGCCAAACTTCTCTCCAAACTTCTCCAAACTTCTCCAAACTTCTCCAAACTTCTCCAAACTTCTCTCCAAACTTCTCTCCAAACTTCTCTCCAAACTTCTCTCCAAACTTCTCTCCAAACTTCTCCAAACTTCTCCAAACTTCTCCTC	GCTCCATACLIACITE CONTROLL CONT

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Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
Peng, J., Malinov, I. and Rubin, E.M.
Direct Submission
Submitted (08-FEB-2003) Genome Sciences, Lawrence Berkeley National
Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
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Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence has been compared to sequences of other species using Vista (http://www-gsd.lbl.gov/VISTA). The results can be viewed at:
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Pred. No. 0;
0; Mismatches 135; Indels 24; Gaps
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Sequencing vector: Plasmid; pUC18
Chemistry: Dye-terminator Big Dye
Assembly program: Phrap version 0.990329.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                    Cercopithecinae; Papio.
1 (bases 1 to 161827)
ChengJ.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
Peng,Z., Malinov,I. and Rubin,B.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   order-orientation of the draft sequence was accomplished
                    hamadryas clone RP41-194B17, WORKING DRAFT SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Funding agent: Programs for Genomic Applications (NHLBI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161827: contig of 161827 bp in length
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Lagan (http://lagan.stanford.edu/) and paired
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/db xref="taxon:9557"
                                                                                              AC139668.1 GI:28273351
HTG; HTGS PHASEL; HTGS DRAFT.
Papio hamadryas (hamadryas baboon)
Papio hamadryas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence Produced by Berkeley PGA
Web site: http://pga.lbl.gov
Center Code: PGABERK
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 179879) Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gun,Q., Gu,X., Guo,D., He,J., Hu,S., Li,Y., Liu,Y., Liu,N., Li,G., Li,J., Li,J., Liu,Y., Liu,N., Li,W	H., Yang, X., Cheng, C., Wang, I., Will, J., Wu, D., Yu, B., Pan, H., Liu, Y., Li, Y., Wu, D., Yu, B., Pan, H., Liu, Y., Li, J., Hang, L., Guo, D. Li, J., Bian, X., Zhang, M., Li, L., Feng, Li, Di, L., Feng, D., Human Genomic Center, Institute cademy of Sciences, Datun Road, Beijir s sequence version replaced gi:7417477 et Center	Center code:Beljing Website:http://hgc.ictp.ac.cn http://www.genomics.org.cn Contact:hcg@igtp.ac.cn Contact:hcg@igtp.ac.cn	Consensus quality: 16726 bases at least 020 Consensus quality: 16726 bases at least 020 Insert size: 148122; sum-of-contigs Quality coverage: 3.56x in Q20 bases;sum-of-contigs Quality coverage: 3.56x in Q20 bases;sum-of-contigs * NOTE: This is a 'working draft' sequence. It currently * NOTE: This is a 'working draft' sequence. It currently * soon sists of 41 contigs. The true order of the pieces * arbitrary. Gaps between the contigs are represented as * runs of N. but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. * 1497: 1596: gap of unknown length * 1497	* 1597 2949: contig of 1353 bp in length * 2950 3049: gap of unknown length * 410 4509: gap of unknown length * 4510 6137: contig of 1628 bp in length * 6138 6237: gap of unknown length * 7285 784: contig of 1047 bp in length * 7385 9013: contig of 1049 bp in length * 9014 10444: gap of unknown length * 914 10544: gap of unknown length * 10545 12153: contig of 1331 bp in length * 10545 12153: contig of 1609 bp in length * 12254 14386: gap of unknown length * 12254 14386: contig of 2133 bp in length * 12254 14386: contig of 2133 bp in length * 14387 14486: gap of unknown length
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clone="RP11-799L19"

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36.6%; Score 1448.2; DB 2;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1456; Conservative 0; Mismatches 13;
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fnote="assembly_name:Contig27"
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note="assembly_name:Contig17"
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note="assembly_name:Contig19"
0598. .22209
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'note="assembly_name:Contig13"
                                                                                      note="assembly_name:Contig12
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Submitted (08-FEB-2003) Genome Sciences, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
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                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Lemur.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence has been compared to sequences of other species using Vista (http://www-gsd.lbl.gov/VISTA). The results can be viewed at:
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Sequencing vector: Plasmid; pUC18
Sequencing vector: Plasmid; pUC18
Chemistry: Dye-terminator Big Dye
Assembly program: Phrap version 0.990329.
* NOTE: This is a "working draft' sequence. It currently
* consists of 1 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Lagan (http://lagan.stanford.edu/) and paired end information.
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                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 190784)
Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.
Peng, Z., Malinov, I. and Rubin, E.M.
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Unpublished
2 (bases 1 to 190784)
Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R. Peng,Z., Malinov,I. and Rubin,E.M.
Direct Submission
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Lemur catta clone LB2-62P23, WORKING DRAFT SEQUENCE.
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/organism="Lemur catta"
/mol_type="genomic DNA"
/db_xref="taxon:9447"
/clone="LB2-62P23"
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Bovidae; Bovinae; Bos.
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                                                                                agcgagacttcctccaaaaaaaaaaaaaaaaaaaaattaagcaaattggacattgcag
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            Query Match 20.6%; Score 816.6; DB 2; Best Local Similarity 73.7%; Pred. No. 2.7e-189; Matches 1386; Conservative 0; Mismatches 389;
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/note="compared to sequence in variant B" /replace="a" variation 14047 /gene="SCD" /note="compared to sequence in variant B"	/replace="t" variation 14578 /gene="SCD" /gene="Compared to sequence in variant B"	replace=-g. variation 14662 /gene="SCD" /gene="SCD" /note="compared to sequence in variant B"		/note="compared to sequence in variant b" /replace="g" varianion 15101	}	variation 15202 /gene="SCD" /note="compared to sequence in variant B" /variace="a"	variation 15284 /gene="SCD" /gene="SCD"		,	variation 1932: /gene="SCD" /note="compared to sequence in variant B" /replace="t"	Query Match 13.2%; Score 521; DB 4; Length 17088; Best Local Similarity 64.9%; Pred. No. 7.7e-117; Matches 1922, Concernative 0. Mismatches 490; Indels 177; Gaps 24;	2164 AAGCAAATTAGACATTGCAGAGAAACCTGAAGGGGGGTCAG	1	OY 2224 GCCACATGCCAAGTACTTCTGAGGCATGACTGGATGAGCTGTCCACATCTGAAATC 2279	QY 2280 ATCCAGTCTTGTTCAAACTTTCACACCGGAGCAGGAGCAGGATGCAGTCTCC 2339	OY 2340 TGGTCACTGGCCAGAGAGTTGGCCTTGACCTGAGACCCAGTGGCCAACAAAGAGCTGCT 2399 179 TGGTCACCGGCCAGAGGCTGGCC-AGACCCCAAGACCTGTGGCCTTCTAGGGAGCTCT 237		QY 2460 GCACTCCGTATTTTCTCCTCTTCCCAGGGAAGGAICCTAGGGCAGTATTTGGGAAAGAC 2519	OY 2520 ATGGGCATGGAAGGACACCGGGTGAATGCATAGCCTGCCT	2576
	Medrano, J Direct Su Submitted	FEATURES Location/Qualifiers Source 117088 /organism="Bos taurus" /mol_type="genomic_DNA"	/db_xret="taxon:9913" /chromosome="26" 117089 117088	oter 1	General Scu." join(1881. 2051,2568. 2850,6720. 6850,8314. 8519, 10099. 10331,13019. 17088)	/gene="SCD" /product="stearoy1-CoA desaturase variant A" join(2025. 2051,2568. 2850,6720. 6850,8314. 8519, 10099. 10331,1301913218)	/gane="SCD" /FC_number="1.14.99.5" /noTe="delta-9 desaturase"	/ocdon start=""" /product="stearcyl-coA desaturase variant A" /protein_id="AAO61569.1"	/ db_xrel="Gl1" 2346.912" 2346.910" 2346.910" 2346.910" 2346.910" 2346.910" 2346.910"	WILFYYLMGALGITAGAHRIWSHRTYKARLPIRVFIJIGYTWAFQNDVFEWRLHKAH HKFSETDADPHNSRGFFFSHVGWILLVRKHPAVKEKGSTLMLSDIABEKUMFGRRYY KPGVILLCFILPILVPWYLMDETFQNSLFFATLFRYALGLNVTWLVNSAAHMYGYRPY DKTINPRENILVSLGAAGGFHNYHHTFPYDYSASEYRWHINFTFFIDGNAAIGLAY DRKKVSKAAILARIKRIGESYKSG"	<pre>variation 6926 /gene="SCD" /note="Compared to sequence in variant B"</pre>	variation 8243		<pre>variation 8646 /gene="SCD" /note="Compared to sequence in variant B" /replace="9"</pre>	<pre>variation 10153 /gene="SCD" /note="Compared to sequence in variant B" /replace="q"</pre>	variation 10213 //gene="SCD" /note="compared to sequence in variant B" /ranlare="compared"	variation 10329 // // // // // // // // // // // // //	variation 13565 /gene="SCD" /note="Compared to sequence in variant B" /replace="t"	variation 13638 /gene="SCD" /note="compared to sequence in variant B"	/replace="c" variation 13757 /gene="SCD"

GENAGGCTCCACAGGCAANANGGAAGACTGGACCACAACAGTSAGG GENAGGCTCCACACACACCCCGGAAAAAGCAAGACTGAGGCACCACACACA	Db 1450 AGAAAGGAACGGAACGCACCAAATCCCTTCGGCCAATGCGCCGA 1509 1510 GCCAATGGCAACGGCAGCACCCCCCTTCGGCCAATGACGACCGCA 1569 1510 GCCAATGGCAACGGCAGGACGACCCCCAATTCCTTCGGCCAATGACGCCCAGA 1569 1510 GCCAATGGCAACGGCAGGACGACCCCCAATTCCTTCGCCCAATGACGCCCGAGA 1569 0y 3661 GTTTACAGAACCCTCATTAGCATTCCCCAGAGGCAGGGCAGGCCGAGGCCGCGCGGTGG 3720 1570 GTCTACAGAACCCCATTAGCATTCCCCAGAGGCAGGGCAGAGGCCGGGCGGG	AX357255 MX35725 MX357255 MX357255 MX357255 MX357255 MX357255 MX357255 MX357255 MX357255 MX357255 MX357255 MX357255 MX357255 MX357255 MX357255 MX357255 MX357255 MX35725 MX3727 MX37	-
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/note="Tandem repeat. Porced join. Gap size estimated be approximately 280bp by restriction digest data." e2058. 62326 / note="Sequence from overlapping clone RP11-228B15.
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153662. .153692
/note="Single clone region. Assembly confirmed
restriction digest data."
                      /chromosome="9"
/clone="RP11-203J24"
/clone_lib="RPCI-11.1"
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Submitted (09-JAM-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:

Cambridgeshire, CB10 18A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Nov 30, 2001 this sequence version replaced gi:16944853.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., pared quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary a covered on numbers given
in the feature table with their source databases: Em:, EMBL: Sw:,
SWISSPROT; Tr:, TREMBL: WD:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                  3938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL157935 164201 bp DNA linear PRI 09-JAN-2002 Human DNA sequence from clone RP11-203J24 on chromosome 9, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
                                                                                                        3818
                                                                                                                                                                                                            ACCECCECECECEACTECTECECACTTTGCCCCTGCTTGCCAGCGGATAAAGGGGGG 3878
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                              363
                                                                                                                                                                                                                                                                                                                                                                      483
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 164201)
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VECTOR: pBACe3.6
this sequence is the entire insert of clone RP11-203J24 The true
left end of clone RP11-379C10 is at 163899 in this sequence. The
true right end of clone RP11-228B15 is at 66809 in this sequence.
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                                                                                                                                    304 GCGGTCGCCGCGAGCCTCGGCCTCTCTCTCTCCCCCCTCCCGCCCTTACCTCCACGCGGG
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/mol_type="genomic DNA"
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AUTHORS TITLE JOURNAL

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tive 0; Mismatches 660; Indels 111; Gaps
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NOTE: This is a "working draft' sequence. It currently consists of 36 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                              Center clone name: RPII-759D18

------ Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 169013 bases at least Q40
Consensus quality: 174569 bases at least Q20
Consensus quality: 17819 bases at least Q20
Betimated insert size: 177488; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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gap of unknown length
contig of 1082 bp in length
gap of unknown length
contig of 1665 bp in length
gap of unknown length
contig of 1065 bp in length
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gap of unknown length
contig of 2262 bp in length
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contig of 2619 bp in length
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      site: http://www.hgsc.bcm.tmc.edu/
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contig of 1569 bp in
gap of unknown leng
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53839: gap of unknown length 61829: contig of 7990 bp in length 61829: contig of 6970 bp in length 68906: contig of 6977 bp in length 68006: gap of unknown length 78800: contig of 9674 bp in length 78800: gap of unknown length 89431: contig of 10651 bp in length 100730: contig of 11800 bp in length 100330: gap of unknown length 112290: gap of unknown length 112200: gap of unknown length 122606: contig of 11360 bp in length 13564: gap of unknown length 13554: gap of unknown length 13554: gap of unknown length 13554: gap of unknown length 147115: gap of unknown length 147315: gap of unknown length 159469: gap of unknown length 15356: contig of 12154 bp in length 15356: contig of 13857 bp in length 17325: contig of 13857 bp in length 17345: gap of unknown length 17345: gap of unknown length 17345: gap of unknown length 17345: contig of 13857 bp in length 17345: gap of unknown length 17345: gap of unknown length 17345: gap of unknown length 17345: gap of unknown length 17345: gap of unknown length
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Pred. No. 1.6e-98;
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/mol_type="genomic DNA"
/db_xref="texon:9606"
/chromosome="3"
/clone="RP11-759D18"
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Best Local Similarity 58.5
Matches 1099; Conservative
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Db 105056 AGTGAGCCGATCACCTGAGGTTCAAACTCACCCCACCCC	http://www.genomecorp.com
09 B91 GCTAATTTTAAAAAATGATTTTGGTATAGGGGGGGGTTCAGCTTGTTGCCCCAGCTCGCTGG 104057 Db 104056 GCTAATTTTTATTGTTGACACATGTGGGGGTTCAGCTGGCTG	1991 GGCAGTGGTGGTCACTCACCACATTCGCCTCCCGGGTTCAAGCAATTCTCCT 1550

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Homo sapiens BAC clone RP11-469M7 from 2, complete sequence. AC005037
AC005037.2 GI:4827310
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                                                                                                                                                                 Gaps
                                                                                                                                                                 96;
                                                                                                                                        Length 175842;
                                                                                                                                       Score 433; DB 9; Length 17
Pred. No. 4.8e-95;
0; Mismatches 670; Indels
:: pBACe3.6.
Location/Qualifiers
Lorganism="Homo sapiens"
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="taxon:9606"
/clone="taxon:9606"
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/clone="taxon:9606"
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Best Local Similarity 58.3
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PRI 30-SEP-2000

us-10-016-725-15_copy_1_3958.rge

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to the right is RPI1-91M5. Actual start of this clone is at base position 1 of RPI1-469M7; actual end is at 190508 of RPI1-469M7. Location/Qualifiers
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                                               FEATURES
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5:1-8. The clone may be obtained either from and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 190508)
Waterston, K.H.
Parterston, K.H.
Submission
Submitted (14-MAY-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://gone.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On May 14, 1999 this sequence version replaced gi:3309089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The clone sequenced to the left is RP11-13J8; the clone sequenced
                                                                  Craniata, Vertebrata, Euteleostomi;
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Washington University Genome Sequencing Center Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                         The sequence of Homo sapiens BAC clone RP11-469M7
                                                                                                                                                   Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: H_NH0469M07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
                                                                Eukaryota, Metazoa, Chordata, Mammalia, Eutheria, Primates; 1 (Dases 1 to 190508) Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- Genome Center
                                                                                                                                                                                                                                 2 (bases 1 to 190508)
Abbott, A. and Le, T.
                                                                                                                                                                                                                                                                                                              3 (bases 1 to 190508)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MO 63108, USA
5 (bases 1 to 190508)
Waterston, R.
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                           sapiens (human)
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                                                 Homo sapiens
                                                                                                                                                                                                                                                                                             Unpublished
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      KEYWORDS
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COMMENT

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	ඊ සි	1568 AGCTGGGACTACAGACTTCCCACCATGCCCAGTTTTT-GTATTTTTAGTAGAGA 1626
9; Conservative	<u>ځ</u>	1627 TGGGATTTCACTTTGTTGGCCAAGCTGGTCTCAAACTTTTTGCTGTCATAATTGTTAA 1686
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66758 ICTGATTTTTTTTTTTTTTTTTTTGAGACAGGGTTTCACTCTGTCACCCCAGGCTGGAG	δδ	1687 CTAȚIGTICCȚITIGCTGAGGIAGGCCCCCAGACCAAAAAAAAAAAAAATAAATICTTAGAATCCA 1746
OY 622 GGCAGTGGCATGGTGACAGCTGAGCAGCCTTGACTTCCTGGGCTCAAGTGATCCTCCT 679	qq	GCCTCCTGCCTCCAGGTTCCCAAAGTGCTGGGATTACAGCCGTGAGCAACCATGCCCCAGCA
680 GCCTCAGCCTCCCAAGTAGCTGGGACTACAAACACGTGTCACCATGCCTGGCTCA	₹ 7	1747 AATCAGTGTGTTGGTTTGACCACTGTCACTTGAGAACCACAGTGTGACCAGGGCCTCAGG L800
Db 66638 GCTTCAGCCTCCCAAGTAGCTGGGACTATAGGCATGTACCACCATGCCTGGCTAATTTTT 66579	g &	TCCGGGCCAGGCGT 1866
735TATITITITITIAAACAGGGTAICACTCTGTIGCGCAGGCTGGAGTACAGTG	3 G	65578 -GIGATTCTCACTTGTTACTTCAAAAATTTGTGAAGAAACTAAGCTATGGCCGGGGAT 65520
66578	ð	1867 GGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCATGTGGATCACCTGAGG 1926
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Search completed: May 13, 2004, 09:06:23 Job time: 24135.2 secs

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dyslipidaemia, atherosclerosis, coronary artery disease, cerebrovascular disease, peripheral vascular disease, inflammation, sinustis, astematis, astematis, astematis, astematis, astematoid arthritis, acne, body weight disorder; obesity, cachexia, anorexia, approxiatic disorder, cancer; cystic fibrosis, pre-menstrual syndrome, diabetes, diabetic complication, genetic polymorphism, ds.
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Jenkins I
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Matches 1834; Conservative
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                                                                                                            TCCCAGGGGAAGGATCCTAGGGCAGTATTGGGAAAGACATGGGCATGGAAGGACACGG
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The present sequence is that of the promoter region of the human stearoyl cot desaturase-1 (hSCD1) gene. The promoter structure is similar to that of the mouse SCD1 promoter and contains conserved regulatory sequences for the binding of several transcription factors. Like the mouse SCD1, the human SCD1 gene is regulated by polyunsaturated fatty acids and cholesterol at the level of gene transcription. The sterol regulatory element binding protein (SREBP) plays a role in the transcriptional activation of the gene. The promoter can be used to identify regulatory elements that modulate and control SCD1 expression in humans, and to identify regulatory proteins that are suitable targets for small molecule intervention to modulate expression of SCD1 in humans. The invention cidentify regulatory proteins that control SCD1 in humans diseases, disorders or conditions relating to serum levels of triglyceride, very low density lipoprotein, high density lipoprotein, low density in propositions relating to serum levels of triglyceride, very lipoprotein, total cholesterol, or production of secretions from mucous membranes, monounsaturated fatty acids, wax seters, etc. Methods for diagnosing and treating such disorders using modulators of SCD1 activity are also provided. These disorders using modulators of SCD1 activity are also provided. These disorders using modulators of SCD1 activity diverse maladies, such as cancer and multiple sclerosis, non-insulindely various seases, and immune disorders as well as cholesterol disorders, eye discenses, and contains and cancer and multiple sclerosis, one insulindely disorders and multiple activity in this dense mediannes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying an agent for treating disorders related to serum levels of fatty acids and glycerols, by contacting screening assay with delta-9 stearoyl-CoA desaturase activity with compound and measuring the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3459 CCCAGCCCCTTCCAGAGAAAAGCTCCCGACGCGGGATGCCCGGGCAGAGGCCCAAGAGGCGCG
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/bound_molety= "CCAAT enhancer binding protein-alpha
(C/EBP-alpha)"
/*tag= k
/*tag= k
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70. .174
*tag= g
/*tag= moiety= "nuclear factor 1"
.76. .180
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'Dound moiety= "nuclear factor Y"
'Atag= i
'bound moiety= "nuclear factor 1"
'19. .437
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(WISC ) WISCONSIN ALUMNI RES I
(UYER-) UNIV BRITISH COLUMBIA.
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31-JUL-2000; 2000US-0221697P.
15-DEC-2000; 2000US-0255771P.
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Miyazaki M;
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  1319 CCCAGCCCCAAACCGGGTCCCCAGCCCCTTCCAGAGAAAGCTCCCGACGCGGGGATGCC 1378
                                                                                                                                                                                                            1439 AGCGAGGAGCTGGCGGCAGAGGGAACAGCAGATTGCGCCGAGGCCAATGGCAACGGCAGGA 1498
                                                                                                                                                                                                                                                                                                              1499 GGAGGTGGCACCAATTCCCTTCGGCCAATGACGAGGCCGGAGTTTACAGAAGCCTCATTA 1558
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/bound moiety= "sterol regulatory element binding protein
(SREBP)"
                                                   3500 GGGCAGAGGCCCAGCGGCGGGGGGGAGAAGAAGCTGAGAAGGAGAAGAAGGGAGAGGGGGG
                                                                                                    1379 GGGCAGAGGCCCAGCGGCGGGTGGAAGAGCAAGCTGAGAAAGCAGAACAGAGGAGGAGGG
                                                                                                                                                           AGCGAGGAGCTGGCGGCAGAGGGAACAGCAGATTGCGCCGAGCCAATGGCAACGGCAGGA
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/note= "polyunsaturated fatty acid response region"
116. .121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             assay; triglyceride; very low density lipoprotein;
high density lipoprotein; low density lipoprotein; cholesterol;
mucous membrane; fatty acid; wax ester; anticholesterolemic;
antiaxteriosclerotic; therapy; ds.
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/bound moiety= "SP1"
102. .169
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/bound_moiety= "SP1"
131. .140
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/bound_moiety= "
151. .154
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Ruben SM; Barash SC, acids encoding human immune/hematopoietic antigen polypeptides, for preventing, diagnosing and/or treating cancers and metastasis. useful for preventing,

Disclosure; SEQ ID NO 38065; 3071pp + Sequence Listing; English

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
proteins and polymucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (1) expression. For
example, they may be used to treat disorders associated with decreased
example, they may be used to treat disorders associated with decreased
that affect the activity of (1) by expressing inactive proteins or to
supplement the patients own production of (1). Additionally, (1)
cupplement the patients own production of (1). Additionally, (1)
polymucleotides may be used to produce the secreted (1), by inserting the
nucleic acids into a host cell and culturing the cell to express the
protein. (1) proteins and polymucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic antigen genomic

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sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
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54.7%; Pred. No. 2.1e-69;
Ative 0; Mismatches 850; Indels 138; Gaps
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The invention relates to genes and their expression profiles are used for: (a) screening modulators of precursor stem cell differentiation into osteoblasts, or bone tissue deposition; (b) diagnosing abnormal caposition of bone tissue, abnormal rate of osteoblast formation or osteoblast; or or monitoring the progression of bone tissue deposition. Specific conditions include postmenopausal osteoporosis, glucocorticoid osteoporosis or male osteoporosis, osteoponia, osteoporosis, glucocorticoid osteoporosis or male osteoporosis, osteoponia, osteoporosis, glucocorticoid osteoporosis or male osteoporosis, osteoponia, osteoporosis, glucocorticoid osteoporosis or male osteoporosis, osteoponia, osteoporosis, sheletal disease linked to breast cancer, mastocytosis, Fanconi syndrome or fibrous dysplasia. The present sequence is that of an osteoplast differentiation associated cDNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                  8192
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TCCCAGCTATTCAGGAGGTTGAGGCAGGAGAATCGTTTGAACCTGGGAGGCAGAGGTTGC
                                                                                                                                 2081 AGTGAAGCGAGATCACACTGCACTCCAGCCTGGGGGA-GAGAGCGAGACTTCCTCTC
                                                                                                                                                                                                              8133 GGTGAGCCAAGATCGCACCATTGCACTCTAGCCTGGGCAACAAGAGCGAAACTCCGTCTC
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9.5%; Score 375.4; DB 6;
Best Local Similarity 55.4%; Pred. No. 5.5e-67;
Matches 1046; Conservative 0; Mismatches 726;
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24-APR-2001; 2001US-0285691P.
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(PROC ) PROCTER & GAMBLE CO.
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WO200157182-A2.	XX NA	56933 TTTTETTTTTTTTTTGACCETTTGAAGGAAGTCACTGTGTGCGCCCACATTTA 56874	업
cytostatic; gene therapy; vacc		1321 TIATACTAAGTGAGAAGTGAGAATTAAGGCTGGAATAGGGCGTTCAGAGTAAATCATGA 1380	δy
Human; immune; haematopoietic;	XX XX	56993 TGACTTTGATCACCTGACTGAGGTAAACTTTGCCAGACTTCTCCATTGTAAAGTTACTCT 56934	d d
Human immune/haematopoietic and	OB	1261 GTTTTCGGAGTTTTATTTTATATTCTGTGACAAATGTGCAGTTTGATGAAAATACAAG 1320	Qy
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KESULI ° AAK69044/c ID AAK69044 standard; DNA; 5491 B: XX	AAK AAK ID XX	1150ATRICTAGGAGIGGAATIGCIGGATICCGGGIAATAITITGACAGGAGGII 1202 57113 AATCCCCTCTATCAGATITGTCTGAGTTTCCTCATGATTAGACTGAGGTTCTGGGTT 57054	6 G
56097 СТСАААААСТААААТАААТА.	අි	ttgatgaccttacagttttggggagtaccgggtaggcatatggtag	7 셤
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	4 0		δλ
56216 GTAGTCCCAGCTACTTGGGAGA	a &	57293 GAATCATTAATAACTAAACTCCATACTTTATTCAGATTTACTCAGTTTCCCCCTAATGTC 57234	QQ Dp
2017 GTAATCCCAGCTACTTGGGAG	λŏ	57353 GGGATTACAGGTGTGCTCCCCTATTATTAACACCTTAGTATGGTACATTTGTCACAAT 57294	d d
56276 AGTGAAACCTTGTCTATTA	· 점	956 TATIGITGAGACAAGGICICACTATGITGCCATGAICCCCCCCACTCCCAAAGT 1015	δλ
56334 GGGAGGCCGAGGCAGGCGGAT	q a ,	896 GITTTAAAAAAGGATTTTTGGTATAGAGGAGTCTTGCTAGTTGCTCAGGCTGTATTTT 955 1 1 1 1 1 1 1 1 1	8 G
56394 TIAATITIGITGCCAAGIGIGG 1897 GGGAGGCCAAGGCATGTGGAT	8 ò	57473 GGAGTGAGCCACTAIGCCCGGCCTAAGTTTTTTAATTTTTCAIAGAGACAAGGTCTCACTA 57414	qq
1846 AATATTCTCCGG	<i>≿</i>		g &
56454 TTATATCAGCATGGACTTACA	q 0	779 GAGTACAGTGGCGTAATAATAGCTCACTGCAGCCTCCCCTCCTGGGCTCAAGCAATC 835	ð í
	名 à	724 IGCCIGGCIGATAITITITITITITITITITITITITITITITITI	& a
565/4 CCCGCCICGACCICTCAAAGIG 1726 AAAAATAAATCTTAGAATCCAA	g &	57653 TICACGCCATICICCTGCCTCCGAGTAGCTGGGACTACAGGCGCCCACCATCA 57594	qa
1670TGTCATAATTGTTAA(₹ :	664 CTCAAGTGATCTCCTCCTCCTCCCTCCCAAGTAGCTGGGACTACAAACACGTGTCACCA 723	ζ
	. A	606 GTTACCCAGGCTGGAGGGCAGGGGATGGTGACAGAGCAGCCTTGACTTCCTGGG 663	충 옵
56694 CCCGAGTAGCTGGGACTACAG	qa k	TICITITCTITTTTTTTTTTTTTTTTGGACGCAGTCTCGCTCT	ž <u>8</u>
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56754 CAATCTTGGCTCACTGCAACT	. d	486 AGTAGGTAGGACTACAGGCACACACAGCCATACCTGGCTAATITITITITITITAATITICA 545	70
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1381 AGCACTITGAATACCAAAATT7 	~ A	366 ATCATATTATTAGAGACAGGTTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGCACAAT 425	δ

GTTAGCCAGGATGGTCTCGGACTCCTGACCTTGTGATCCG 56575 recresdairacassecricasceacededededescaerrr 56515 AAAAATACAAAAATTAGCTAAGTGTGGTGGCGCATGCCT 2016 ACCACTGCACTCCAGCCTGGGGAGAGAGCGAGACTTCCT 2136 craccrecriraaggecagarareracacaggrrirger 56815 ggàgarridcciarrcicccrrárirarrcarccar 56455 agdiartratrtatacrticdgarardarcicaaacrac 56395 3GCCAGGCGTGGTGGCTCACACCTGTAGTCCCAGCACTTT 56335 TTTCGCCTCCCGGGTTCAAGCAATTCTCCTGCTTCAGCCT 1560 AAATCAGTGTGGTTTGACCACTGTCACTTGAGAACCA 1785 aggrgaggcaggaartrerrgaacccgggaggcaggg 2076 AAGAGTCTTGCTCTTTCACCCTGGCTGGAGGGCCAGTGGTG 1500 ACTATTGTTCCTTTTGCTGAGGTAGGGCCCCCCAGACCAAA 1725 GAGTAGAGGTGATCTCTGCTCGAAAGAGAAATAGAATGAA 1845 IAAGGAGCIIGGCIGIAAACAAAIAAIAAAAAAICACAA 1440 GGCACTTCCCACCAGCTGATTTTTGTATTTTAG 1620 SECCAGGCGTGGTGGCTCATGCCTGTAATCCCAGCACTTT 1896 STIGGCCAAGCTGGTCTCAAACTITTTGC-------;; immune/haematopoietic antigen; cancer; cine; metastasis; ds. ntigen genomic sequence SEQ ID NO:23856. AAATTT 56071 AAGAATT 2163 BP.

2001WO-US001354. 2000US-0179065P. 2000US-0184664P. 2000US-018658P. 2000US-018658P. 2000US-018678P. 2000US-019076P. 2000US-0218123P. 2000US-0218132P. 2000US-0218486P. 2000US-0218486P. 2000US-021868P. 2000US-021868P. 2000US-02189P. 2000US-02189P. 2000US-02189P. 2000US-02189P. 2000US-02189P. 2000US-02189P. 2000US-022828P. 2000US-02384P. 2000US-02384P. 2000US-0231414P. 2000US-0231414P. 2000US-0231414P. 2000US-0231414P. 2000US-0231414P. 2000US-0231414P. 2000US-023189P. 2000US-023138P. 2000US-023141P. 2000US-023141P.	000US-0233064E 000US-0234223E 000US-0234224 000US-0234274E 000US-023499F 000US-02354848 000US-02358484E 000US-0235836E
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                                                                                                          AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polyuucleotides may be used in the prevention, diagnosis and
carpension of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally. (I)
polynucleotides may be used to produce the secreted (I), by inserting the
nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic-derived cells AAK64703
concers and cancer human immune/haematopoietic-derived cells AAK64703
concers from the present invention. AAK54942 to AAK54595 and AAM82169
represent sequences used in the exemplification of the present invention
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                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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2071 CAGAGGTTGCAGTGAAGCGAGATCACACCACTGCACTCCAGCCTGGGGGAGAGAGCGAGA 2130
                                                   2066 CGGAGCTTGCAGTGAGCCGAGATTATGCCACTGCACTCCAGCCTGGACCACAGAGCAAGA 2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovoscular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic; anti arthritic; nephrotropic; anticoagulant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence #331 encoding novel human enzyme polypeptide.
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2000US-025267P.
2000US-025268P.
2000US-025270P.
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2000US-0198123P.
2000US-0205515P.
2000US-0209467P.
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609 ACCCAGGCTGGAGGGCAGTGGCATGGTGACAGCTGAGCAGCCTTGACTTCCTGGGCTCAA

GGTCAGGCTGGT

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6231 AGCTGGGGTTACAGGCATGTGCCACCACGCCCGGCTAATTTTTGTATTTTTA------549 TAIGTATICATTICTTICTTITITIGTIGTIGTTGTTTTGAGATAGGGTCTCACTTTGTT 668

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GTGATCCTCCTCCCTCCCAAGTAGCTGGGACTACAAACACGTGTCACCATGCCT

6065 GGCCTTTTTTTTTTTTTTAGALGAGTTTCGCTCTGTCACCCCAGACTGGAGTGCAGG

GGCTGATATTTTTTTTTTTGAAACAGGGTATCACTCTGTTGCCCCAGGCTGGAGTACAGTG

GCGTAATAATAGCTCACCTGCAGCCTC-CCCTCGGGCTCAAGCAATCCGCTGGGCCTCAG

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CATCCTGAGTAGCTGGGACTACAGGCTTGTGCCACCCAGCTAAGTTTTAAAAAAT

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968 AAGGICICACIAIGIIGCCAIGAICCCCCCACCICCAACIICCCAAAGIGCICAITAIC 5829 caag------rearceccececcecciccaaacierragaariara 1028 IGTICALTAGICAGITGACAGACATTIAGGITGTITCCACTITITGACCATTAIGAATAA

908 GATTITIGGTATAGAGGAGGTCTTGCTATGTTGCTCAGGCTGTATTTTTATTGTTGAGAC

5785 GGCGTGAGCCACGGCATCTGAGTGCATGAACTATTTAAAGGGCCCAGTCATTGATCTAAAT TACTCCAGTGAATATTCATGTATACATTTGTGTGGGCATATGTTTTCATTTCTGTTGGGT Greengragerraarreacegecerraggrrrargeacaggrreargeacargrrerage TTATATCTAGGAGTGGAATTGCTGGATCCCGGGTAATATTTTGACAGGCAGAGTTCAGGG

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Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
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                                                                                                                                                                                                                                                    Ruben SM;
                                                                              2000US-0249297P.
2000US-0249299P.
2000US-0249300P.
2000US-0250160P.
                                                                                                               2000US-0250391P.
2000US-0251030P.
2000US-0251988P.
2000US-0256719P.
2000US-0249214P.
2000US-0249215P.
2000US-0249217P.
2000US-0249217P.
2000US-0249218P.
2000US-0249218P.
                                                              2000US-0249264P.
2000US-0249265P.
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2000US-0251868P.
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                                                                                                                                                                                                        11-DEC-2000; 2000US-0254097P
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                                                                                                                                                                                                                                                    Barash SC,
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The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU22814), and the cDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. awide range of manunodeficiency disorders (e.g. Alzheimer's disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disorders (e.g. arthritis) cardiovascular disorders (e.g. alzheimer's disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. infectious disorders (e.g. infercility) and infectious disorders (e.g. infercility) and infections disorders (e.g. infercility) and infections on also be used in gene therapy. AAS41685-AAS42192 represent DNA sequences encoding for the novel human enzyme polypoptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly town WIPO at ftp.wipo.int/published_pct_sequences

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Db 5569 AAGICTTGCAGCTAGGCATGGGAGCTCACACTGTAATCTCAGTGCTTTGGGAGGCTGAG	Qy 1327 TAAGTGAGAATTAAGGCTGGAATAGGCGTTCAGAGTAAATCATGAAGCACT D 5509 GCAGGAGGATCGCTTGAGGCCAGGAGTTTGAGACCAGCCTGGGGAACATAGCGAGAACCTTGAGGCCCAGGAGATTTGAGACCAGCCTGGGGAACATAGCGAGAACCTTGAGGCCCT	Qy 1387 ITGAAIACCAAAAITAAGGAGCTIGGAAAAAAAAAAAAAA	Db 5449 AICTCTAIGAAATAAACAAATAAAAAAAAAGTGTAGAAATATCTTGCTTTTCTTTTCTT	Ov 1447 TTTTTTTTGAGAAAGAGTCTTGCTCTTTCACCCTGGCTGG	5389	Qy 1507 CAGCICACTGCAACTITCGCCTCCCGGGITCAAGCAATICICCTGCTICAGCCTCCCAAG	Db 5329 CAGCTCACCACAACTTCAGGTTCAGGATTCTCCTCCCTCAGCCTCAAG	Ov 1567 TAGCTGGGACTACAGGCACTTCCCACCATGCCCAGCTGATTTTTGTATTTTTAGTAGAGA		
invention can also be used in gene thereby. Anstroso Anstros represent	nivention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences	Sequence 9742 BP; 2382 A; 2564 C; 2516 G; 2280 T; 0 U; 0 Other;	Length 9742;	ches 1043; Conservative 0; Mismatches 631; Indels 178; Gaps 12;		6351 TTTTCTTTGAGATGGAGTTTCACTCTTGTTGCCCAGGCTGGAGTGCTGTGGGCGCTATCTT 6292	429 AGCTCACTGTAACCTCTAAACTCCTGGGCTCAAGTGATCCTACCTCACCTCCAGAGT 488	6291 GÉCTCATTGCAACCTCCGCCTCCCGGGTTCAAGCAATTCTCCTGCCTCAGCCTCCTGAGT 6232	489 AGCIAGGACTACAGGCACACACACATACTGGCTAATTTTTTTTT	

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GAAGAAAAACTTGGGAAAATGAAGCATGTTTAGAAATCAGCAAG-AGTGCAGGGGTTTTT 1266

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-nagagaartriaaggaactrigctaacggrigcacaggcdaggaagraraggcagctaagaa CGGAGTITTATTITATATTCTGTTGACAAATGTGCAGTTTGATGAAGATACAAGTTATAC 5390

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                                    5209 CGGGGTTTCACTATGTTGACCAGGCTGGTCTCGAACTCCTGACCTTGTGATCTGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5029 AGAATAGCAAGACAGTTACTCAAGATCATTCATATAACCGGTTAGTTGTAATTCCAACA
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                                                                                                                                     -TIGTAACTAITGTICC
                                                                                                                                                                                                  5149 TCGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCTCGCCTGGCCGTCTTGGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCATGTGGATCACCTGAGGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTAGCTAAGTGTGGCGCATGCCTGTAATCCCAGCTACTTGGGAGGGTGAGGCAGGAG
1627 IGGGATTICACTITIGITGGCCAAGCIGGTCTCAAACTITITIGGIGTCATAAITG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1757 TTGGTTTGACCACTGTCACTTGAGAACCACAGTGTGACCAGGGCCTCAGGAGT-
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/product= "PACAP protein"
/note= "Includes exons and introns"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present genomic sequence is that of human pituitary adenylate cyclase activating polypeptide (PACAP). This gene is localised to the short arm of chromosome 18p11 and synthesised in the retinal ganglion cells. The gene Has a gisolated from lymphocytes of individuals. The coding region of the gene has a dinucleotide repeat polymorphism marker known as Wildo and am STS marker, ADCYAPI is located in the 3'UTR. These markers are useful to map the gene physically and genetically to the chromosome 18. This sequence can be used to design probes for detecting the presence or absence of a mutation in the wild type PACAP gene. It is also useful for genetic diagnosis of neuropsychiatric disorders like bi- polar affective disorder(BP-I) and schizoaffective disorders like bi- polar which are more valid than current clinical diagnosis based on clinical observation and subjective reports. It is used for identifying compounds that modulate PACAP gene expression which are useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20031 ACAACTITATTTATTTATTTATTTTAAGAAGAGTCTCGCTCTGTTGCCCAGGCTGG
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                                                                                                                                                                                                                                                                                                                                      Use of a gene linked to the region of a chromosome associated with neuropsychiatric disorders, especially for diagnosis of bi-polar affective disorder and schizoaffective disorder manic type.
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8.6%; Pred. No. 4.8e-63;
ve 0; Mismatches 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2A-2U; 99pp; English
                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC. (REGC ) UNIV CALIFORNIA.
                                                                                                       99WO-US007401
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Matches 522; Conservative
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                                                                                                       02-APR-1999;
                                                               14-0CT-1999
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20447 ATCATACGGGCGGGGGGGGGGGCTGGTAATCCCAGGATTTGGGAGGCCGAGG
                               10507 TGGGCGGATCAC-GAGGTCAGGAGATCGAGACCATCCTGGCTAAAACGGTGAAACCCCG
                     1909 CATGTGGATCACCTGAGGTCAGGAGTTCAAAACCAGCCTGGCCAACATGGTGAAAACCCCG
                                                TCTCTACTAAAAATACAAAAATTAGCTAAGTGTGGTGGCGCATGCCTGTAATCCCAGCT
                                                            ACTIGGGAGGGIGAGGAGGAGAATITCTIGAACCCGGGAGGCAGAGGIIGCAGTGAAGC
                                                                                        20625 ACTCGGGAGGCTGAGGCAGGAGATGGCGTGAACCCGGGAGGCGGGAGCTTGCAGTGAGCC
                                                                                                      "Human glycogen synthase kinase 3 alpha"
                                                                                                                                             20745 AAAAAAAAAAAAAAAAAAGGAATCATACTTGGAAAGGGAA 20785
                                                                                                                                 2189
                                                                                                                                                                                                                                                        hyperproliferative disorder; developmental disorder; ds
                                                                                                                                 AAAAACAAAAGAATTAAGCAAATTAGACATTGCAGAGAAA
                                                                                                                                                                                                                       Human glycogen synthase kinase 3 alpha genomic DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense compound 8 to 30 nucleobases in length comprising a compound that is targeted to a nucleic acid molecule encoding glycogen synthase kinase 3 alpha, useful for the treatment of e.g. diabetes and hyperproliferative disorders.
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8.8%; Score 349.8; DB 4;
Best Local Similarity 55.2%; Pred. No. 6.4e-62;
Matches 1016; Conservative 0; Mismatches 742;
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OY 1724 ANAAATAAATCTTAGAATCCAAATCAGTGTTTGGT Db 4967 GAGCCACCACGCCTGGCCCTGGCCTATCCTT QY 1784 CACAGTGTCACCAGGCCTCAGGAGTAGATGTTCTC Db 5020 AAAATCACAGGCCCATTTGCCTTTACATGTCAGC QY 1844 AAAATTCTCCGGGCCAGGCGTGGTGGCTCATGCCTG QY 1844 AAAATTCTCCGGGCCAGGCGTGGTGGCTCATGCCTG QY 1844 AAAATATTCTCCGGGCCAGGCGTGGTGGCTCATGCCTG	5080 1904 5140 1935 5200 1995	OY 2055 TCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGA 	XX XX XX XX XX XX XX XX XX XX XX XX XX	XX XX XX XX PD 02-AUG-2001. XX FF 17-JAN-2001; 2001WO-US001339. XX XX X3 1-JAN-2000; 2000US-0179065P. PR 24-FEB-2000; 2000US-018658P. PR 24-FEB-2000; 2000US-018659P. PR 14-MAR-2000; 2000US-0186350P. PR 17-MAR-2000; 2000US-0189874P. PR 17-MAR-2000; 2000US-0189874P. PR 19-MAY-2000; 2000US-019812P. PR 19-MAY-2000; 2000US-0209467P. PR 26-JUN-2000; 2000US-0209467P. PR 26-JUN-2000; 2000US-0215135P. PR 07-JUN-2000; 2000US-0215135P. PR 07-JUN-2000; 2000US-0215135P. PR 11-JUL-2000; 2000US-0215135P. PR 11-JUL-2000; 2000US-0216880P. PR 11-JUL-2000; 2000US-0218290P. PR 11-JUL-2000; 2000US-0218290P. PR 26-JUL-2000; 2000US-0220963P. PR 26-JUL-2000; 2000US-0220963P. PR 26-JUL-2000; 2000US-0220963P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic; gene; ds.
    1501 TGATCTCAGCTCACTGCAACTTTCGCCTCCCGGGTTCAAGCAATTCTCCTGCTTCAGCCT
                                3685 CGATCTCAGCTCACTGCAAACTCCACCTCCCGGGTTCAAGAGATTCTCCTGCCTTAGCCT
                                                                                             CCCAAGTAGCTGGGACTACAGGCACTTCCCACCATGCCCAGCTGATTTTTGTATTTTTAG
                                                                                                                           CCTGAGTAGCTGGGATTACAGGCGTGCACTACCGTGCCTGGCTAATTTTATATTTTTAA
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                                             human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3745 CCTGAGTAGCTGGGATTACAGGCGTGCACTACCGTGCCTGGCTAATTTTTATATTTTTAA
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                         sednences of
                                                                                                                                                                                                                     Sequence 13216 BP; 3041 A; 3400 C; 3243 G; 3532 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                8.8%; Score 349; DB 4; Length 13216; 70.0%; Pred. No. 9.4e-62;
                                                                                                                                                                                                                                                                                                                0; Mismatches 210; Indels
                           The present invention provides the protein and coding
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ABV52505 standard; cDNA; 396 BP
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Matches 516; Conservative
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                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 2666; 766pp; English
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2000US-0249210P
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                                                                       RESULT 13
                                                                                      AAL0512
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                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid molecule (I) comprising a nuclectide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (C) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient
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                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAGCAAGAGTGCCAGGGGTTTTTTCGGAGTTTTTATTTTTATATTCTGTTGACAAATGTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 8.8%; Score 348.6; DB 5; Length 396; al Similarity 98.9%; Pred. No. 5.1e-62; 351; Conservative 0; Mismatches 4; Indels 0.
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                                  Human prostate expression marker cDNA 52496.
                                                                                                                                                                                                                                                                                              MILLENNIUM PREDICTIVE MEDICINE INC.
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reproductive system related antigen; reproductive system disorder;
88 GCTGGAGGGCAGTGGTTGATCTCAGCTCACTGCAACTTTCGCCTCCCGCGTTAA 34
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                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCAAGTAGCTGGGACTACAGGCACTTCCCACCATGCCCAGCTGATTTTTGTATTTTAG
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       CTGAGGTCAGGAGTTCAAAACCAGCCTGGCCAACATGGTGAAAACCCCCGTCTCTAAAA
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TACAGATGGGGTTTCACCATGTTGGTCAGGCTGGTCTCGAACTCCTGACTTCATGATCCG 3862
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                                                        AATCCAAATCAGTGTGTTTGACCACTGTCACTTGAGAACCACAGTGTGACCAGGGC
                                                                                                                                                                  ---GCTAATTTTTTTTTTGTACAGACAGATTTCTCCATGTTGCCCAGGCTGATCTGGAA
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ID AAS42014 standard; DNA; 6437 BP.
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16-MAR-2000;
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19-MAY-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of 973 minan testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and agastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
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Pred. No. 2.4e-61;
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465566/50

Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.

Disclosure, SEQ ID NO 2140; 1180pp; English.

The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the CDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the

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diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. ALDS) autoimmune disorders (e.g. arthritis) arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. inflammatory ABS41689-ABS42192 represent DNA sequences encoding for the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 2.1e-61;
0; Mismatches 625; Indels 180;
                                                                                                                                                                                                                                                                            Sequence 6437 BP; 1690 A; 1641 C; 1586 G; 1520 T; 0 U; 0 Other;
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Best Local Similarity 56.7%;
Matches 1052; Conservative
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	cagggaaraaaacttgggaaaatgaagcatgtttagaaatcagcaag-agtgcaggg 	TITITCGGAGTITIATATITATATICCTGTTGACAAATGTGCAGTTTGATGAAGATACAAGT 	TATACTAAGTGAGAAGTGAGAATTAAGGCTGGAATAGGGCGTTCAGAGTAAAATCATGAA TATACTAAGAAGAAGAAGAAGAAGAAAAAAAAAA	GCACTTTGAATACCAAAATTAAGGAGCTTGGCTGTAAACAAAAAAAA	AAATAAGTG CTCTTTCAC	TICTITITITITITIAGACAGAATCTCACTCTGTTGCCCAGGCTGGAGTGCATGTGT	GAICTCAGCTCACTGCAACTITGGCCTCCGGGFTCAAGCAATICTCCTGCTTCAGCCTC	CCAAGTAGCTGGGACTACCGGCACTTCCCACCATGCCCAGCTGATTTTTGTATTTTTAGT	CTGGTCTCA	credrata		Acadgrere	TICCITITIGCIGAGGIAGGCCCCCAGACCAAAAAAAAATAAAICTIAGAAICCAAAITCAG 	AACCACAGT		agaggigatctctgctcgaaagagaaatagaatgaaaatattctccggcccaggcgtg	стёттаёа́а	GTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCATGTGGATCACCTGAG	TTGGGAGGT	GTCAGTAGTTAATAAATAGCCTGGTCAACATGTTGAAACCTCATCTCTACTAAAAAATACA	CTGTAATCC	AAAATTAGCCAGGCGTGTGGCACCCACCTATAGTCCCAGCTACTTGGGGGGCTGAGGC	AGGAGAATITICITGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGATCACCACCACTGCA	GGTTGCAGG	CTCCAGCCTGGGGGAGAGAGAGACTTCCTCAAAAAAAAAA
CCAGTGAGG	AAATGAAGO ACTTGCTAA	ATTCTGTT(ATTAAGGC	AGGAGCTT	ACAAATAAA	GAATCTCA	110gccrcc 10gccrcrc	SCACTTCCC	TGGCCAAG	TGACCAGG	SCIGICATA	screecarr	CCCCAGACO	rcactrgag	TACTCAAG	AAAGAGAAA 	AGGATGCAC	CCCAGCACT	CTAGCGCT	TGGTCAAC	GCGCATGC	GCACCCAC	GAGGCAGA	SGAGGTGGA	GAGACTIC
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Search completed: May 12, 2004, 19:47:11

Job time : 2140.36 secs

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ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXPI
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                                                                                                                                                           Sequence 3, As
Sequence 3, As
Sequence 7, As
Sequence 1, As
Sequence 6, As
Sequence 6, As
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                                 Sequence 1, A
Sequence 10,
Sequence 3, A
Sequence 20,
                                                                                                       Sequence 21,
Sequence 22,
Sequence 3, A
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 Sequence
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Pred. No. 4.9e-77;
0; Mismatches 742;
                               US-09-345-882-1
US-09-488-856A-10
US-09-108-006C-3
US-08-724-394A-21
US-08-724-394A-21
US-09-818-512-3
US-09-818-512-3
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US-09-146-053-6
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JS-09-435-739-42
                                                                                                                                                                                                                                                                                                        US-09-791-211-10
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APPLICANT: Robert McKay
APPLICANT: Madeline M. Butler
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION:
FILE REFERENCE: RTS-0115
CURRENT FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 88
                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
US-09-488-856A-10
; Sequence 10, Application US/09488856A, 2 betent No. 6316259
; GENERAL INFORMATION:
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Best Local Similarity 55.2%;
Matches 1016; Conservative
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NAME/KEY. CDS
LOCATION: (1864) ... (5974)
NAME/KEY: CDS
LOCATION: (7902) ... (8032)
NAME/KEY: CDS
LOCATION: (8121) ... (8227)
NAME/KEY: CDS
LOCATION: (9197) ... (9294)
NAME/KEY: CDS
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NAME/KEY: CDS
LOCATION: (9898)...(10084)
NAME/KEY: CDS
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CDS
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LENGTH: 12394
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NAME/KEY:
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Sequence 3, Application US/097906
Sequence 3, Application US/097906
Sequence 3, Application US/097906
Seatest No. 6329188

BEALELLOANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEA
TITLE OF INVENTION: USCATED HUMAN PROTEANS,
TITLE OF INVENTION: USCS THEREF
FILE REFERENCE: CLO01151CIP
CURRENT APPLICATION UNMBER: US/09/797,906
CURRENT FILING DAITE: 2001-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 84495
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LOCATION: (1)...(84495)

CTHER INFORMATION: n = A,T,C

US-09-797-906-3
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US-09-797-906-3/c
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11454	RESULT 3 US-09-108-006C-3/C ; Sequence 3, Application US/09108006C ; Sequence 3, Application US/09108006C ; Patent No. 6524613 ; GENERAL INFORMATION:
	QY 1159 AGTGGAATTGCTGGATCCCGGGTAATATTTTGACAGGCAGAGAAAACT 1218

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1456 TCCCAGCCAGGTGCGCTCACGCCTGTAATCCCAGCACTTTGGGAGATCGAAACGGG 1397
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                                                                                                                                                                                                                                                                                                                                                                       TGGGAGGGTGAGGCAGGAGAATTTCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAG
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                                                                                                                                                   1396 cagarcaccreaggreaggriccagaccagccregccregccaacarggreaaacccgrere
                                                                                                                                                                                                                           1973 TACTAAAATACAAAAA-TTAGCTAAGTGTGGTGGCGCATGCCTGTAATCCCAGCTACT
                                                                                   1913 TGGATCACTGAGGTCAGGAGTTCAAAACCAGCCTGGCCAACATGTGAAACCCGT
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STREET: 30500 No. 6025183thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
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APPLICANT: Sakut, Haim
APPLICANT: Shadi, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 48334

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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NAME: Montgomery, llene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/814,09
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Patent No. 6025183
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 800
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DESCRIPTION:
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US-08-814-095-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1734 AICTTAGAATCCAAAICAGTGTGTTGGTTTGACCACTGTCACTTGAGAACCACAGTGTGA 1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1794 CCAGGGCCTCAGGAGTAGAGGTGATCTCTGCTCGAAAGAGAAATAGAATGAAATAT-TC 1852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 TCACAGCTGCCCGTGTCTGGTATTCACTATCTGCCAATGCATTAGAAACCTCTAAC 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1876 ritarieratirianáakokássirorrisórichstókocokásokásasásasásásokásakó 1817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIAGCIGGGACTACAGGCACTICCCACCATGCCCAGCTGATTTTTGTATTTTAGTAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.1%; Score 322.4; DB 4; Length : Best Local Similarity 68.3%; Pred. No. 1.8e-70; Matches 496; Conservative 0; Mismatches 216; Indels
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
RENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/09/108,006C
FILING DATE: 30-Jun-1992
CLASSIFICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/054,837
FILING DATE: 05-AUG-1997
APPLICATION NUMBER: 60/064,996
FILING DATE: 10-NOV-1997
APPLICATION NUMBER: 60/074,497
FILING DATE: 12-FEB-1998
APPLICATION NUMBER: 60/074,497
FILING DATE: 30-APR-1998
ATTORNEY/AGENT INFERE: PARR-1998
ATTORNEY/AGENT INFERE: PARR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Friebel, Thomas
REGISTRATION NUMBER: 29258
REFERENCE/DOCKET NUMBER: 7991-015-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 14444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COCATION: 71...114
OTHER INFORMATION: Exon 1
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-108-006C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 3805 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 215-504-4545
TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3:
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LOCATION: 24090..25177
LOCATION: 24090..25177
LIDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "(translation start:
OTHER INFORMATION: /4110) "
OTHER INFORMATION: /40ne= "ACHE"
OTHER INFORMATION: /60ne= "ACHE"
OTHER INFORMATION: /10umber= 2
FEATURE:
NAME/FEX: exon
LOCATION: 25524..26009
LDENTIFICATION METHOD: experimental
OTHER INFORMATION: /40ridence= EXPERIMENTAL
OTHER INFORMATION: /40ridence= EXPERIMENTAL
OTHER INFORMATION: /40ridence= EXPERIMENTAL
OTHER INFORMATION: /10umber= 3
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NAME/KEY: exon
LOCATION: complement (34528..34895)
OCHER INFORMATION: gene" arrenite resistance
OTHER INFORMATION: /gene" "AR"
OTHER INFORMATION: /gene" "AR"
FEATURE:
NUMBER INFORMATION: /gene" "AR"
NAME/KEY: promoter
LOCATION: 4089..22464
OTHER INFORMATION: /function= "ACHE Promotor"
OTHER INFORMATION: /standard_name= "ACHE Promotor"
                                                                                                                 LOCATION: 22465..22537
OTHER INFORMATION: /function= "non-translated"
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 1
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: terminator
LOCATION: 27385.27387
FEATURE:
NAME/KEY: exon
LOCATION: 28008..28129
IDBNTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /gene= "ACHE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: exon
LOCATION: 27005..27274
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME. SECTION: 27255..28007
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /mumber= 5
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LOCATION: complement (34092..34358)
OTHER INFORMATION: /gens= "AR"
OTHER INFORMATION: /number= 2
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: terminator
LOCATION: 28129..28131
                                                                                                    FEATURE:
NAME/KEY: exon
LOCATION: 22465
                                                                                                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: 24090
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NAME/KEY: exon
LOCATION: compl
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LOCATION: comp.
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complement (33493..33591)

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9802 ICTITITCTITIGAGAGGGAGTCTCGCTCTATCGCCCAGCGGGGGGCACAGAT 9861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
8.1%; Score 321; DB 3; Length 35060;
Best Local Similarity 68.8%; Pred. No. 1.3e-69;
Matches 511; Conservative 0; Mismatches 205; Indels 27
                                                                                                                                                                                                                                                                 FEATURE:
NAWE/KEY: exon
LOCATION: complement (32569..32628)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 7
FEATURE:
NAME/KEY: exon
LOCATION: complement (32386..32468)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /gene= "AR"
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LOCATION: complement (31131..31284)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 11
FEATURE:
NAME/KEY: exon
LOCATION: complement (30816..31011)
                                                                                 LOCATION: complement (33297..33408)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 5
FEATURE:
NAME/KEY: exon
LOCATION: complement (32959..33094)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /mumber= 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: exon
LOCATION: complement (31363..31534)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: exon
LOCATION: complement (31894..32080)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
FEATURE:
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COCATION: complement (29664..29856)

COTHER INFORMATION: /gene= "ARS"

US-08-814-095-7
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NAME/KEY: exon
LOCATION: complement (30187..30274)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: complement (30816..31011)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
  /gene= "AR"
/number= 4
OTHER INFORMATION:
OTHER INFORMATION:
                                            RATURE:
NAME/KEY: exon
LOCATION: compl
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LOCATION: compl
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NAME/KEY: exon:intron junction
LOCATION: (348578)...(348579)
OTHER INFORMATION: exon 10:intron 10
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LOCATION: (220360)...(220459)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (222717)...(222816)
OTHER INFORMATION: n = A,T,C or G
LOCATION: (223981)...(224080)
OTHER INFORMATION: n = A,T,C or G
CACATION: (223981)...(224080)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: 154217
OTHER INFORMATION: unknown
NAME/KEY: misc feature
LOCATION: (164037)...(164136)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (230157) ... (230256)
OTHER INFORMATION: n = A,T,C or G
NAMEXEY: misc_feature
LOCATION: (232299) ... (232398)
OTHER INFORMATION: n = A,T,C or G
                          NAME/KEY: ungure
LOCATION: 145507
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 151967
OTHER INFORMATION: unknown
NAME/KEY: misc_feature
LOCATION: (151967)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (186224)...(186323)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
LOCATION: 202703
OTHER INFORMATION: unknown
NAME/KEY: misc feature
LOCATION: (202771)...(202870)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (227487)...(227586)
OTHER INFORMATION: n = A,T,C or G
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LOCATION: (299248)...(299249)
OTHER INFORMATION: exon 9:intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (151129)...(151130)
OTHER INFORMATION: exon 5:intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (206246)...(215602)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (174657)...(174756)
OTHER INFORMATION: n = A,T,C or
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LOCATION: (195242)...(195341)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (218126)...(218225)
OTHER INFORMATION: n = A,T,C or
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OTHER INFORMATION: n = A,T,C or
NAME/FRST misc.feature.
LOCATION: (238789)...(248788)
OTHER INFORMATION: n = A,T,C or
     = A,T,C or
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LOCATION: (151129)...(151130)
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OTHER INFORMATION: exon 1C
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APPLICANT: Kenneth W. Dobie
APPLICANT: Mark P. Roach
TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
FILE REFERENCE: RTS-0340
CURRENT APPLICATION NUMBER: US/10/027,983
CURRENT FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 11
LENGTH: 392000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10461 TAGTGAGCTGAGATTGCACCATGGCACTCCATCCTGGGCCAACAGGAGAAACTCCGTCT 10520
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9862 CTGGGCTCACTGCAACCTCTGCCACCCAGGTTCAAGCAATTTTCCTGTGTCAGCCCCA 9921
                                                                                       9922 Aaradcicecentraccadreccaccacadareccaderaaririraraariricadrada 9981
                                                                                                                                                                                                                                                                                                                                                                                                                         1733 AATCTTAGAATCCAAATCAGTGTGTTGGTTTGACCACTGTCACTTGAGAACCA-----
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NAME/KEY: unsure
LOCATION: 137740
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 137742
OTHER INFORMATION: unknown
NAME/KEY: misc_feature
LOCATION: (138122)...(138221)
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                                                                                                                     Length 392000;
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                                                                                                                     Score 319.8; DB 4; Length
Pred. No. 9.6e-69;
0; Mismatches 217; Indels
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; NAME/KEY: intron
; LOCATION: (348579) ...(381838)
; COCHION: 13487101: intron 10
; NAME/KEY: intron: exon junction
; LOCATION: (386185)
; COCHION: (386185)
; OTHER INFORMATION: intron 11:exon 12
US-10-027-983-11
                                                                                                                       Query Match
Best Local Similarity 67.2%;
Matches 533; Conservative (
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RESULT 6 10S-09-813-817-3/c 'Sequence 3, Application US/09813817 'Patent No. 6340583

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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1178
CURRENT APPLICATION NUMBER: US/09/813,817
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FREUSEQ for Windows Version 4.0
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Pred. No. 2.2e-68;
0; Mismatches 264;
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Best Local Similarity 66.7
Matches 561; Conservative
                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                 SEQ ID NO 3
LENGTH: 59065
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ORGANISM: Human
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US-09-804-471A-3
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APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLOO178BIN

CURRENT APPLICATION NUMBER: US/09/978,197

PRIOR APPLICATION NUMBER: 09/813,817

PRIOR FILING DATE: 2001-03-22
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                               Sequence 3, Application US/09978197
Patent No. 6403353
                                                                          11629 A 11629
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; ORGANISM: Human
US-09-978-197-3
                                                                                                                     RESULT 7
US-09-978-197-3/C
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126675 INICICCCCCTITCTCCCAAAATATGGCAGACTCTTCTGTCCCCTAGTCATTCTCATATA 126734
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APPLICANT: WEBSTER, MAXION et al
APPLICANT: WEBSTER, MAXION et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOO1164
CURRENT APPLICATION NUMBER: US/09/804,471A
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1929 AGGAGTTCAAAACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAATACAAAA 1988
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                                                      11867 AGGAGTTCGAGACTAGCTTGGCCAACATGGCAAAACCCCCATCTCTACTAAAATA-TAAA
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; LOCATION: (1)...(174493)
; OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3
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126974

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APPLICANT: BOUGHELET, Lydie
APPLICANT: BOUGHELET, Lydie
APPLICANT: BOUGHELET, Lydie
APPLICANT: BOUGHELET, Lydie
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REPERENCE: GENSET, 031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR PILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
SEQ ID NO: 140
SOFTWARE: Patent.pm
                           26555 TAGAGATGGGGTTTCACCATGTTGAAGCATTTAAGAAAAGGGGTTAGGAGGAGGAGGAGAAGACA 126614
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1621 TAGAGATGGGGATTTCACTTTGTTGGCCAAGCTGGTCTCAAACTTTTTGCTGTCATAATTG 1680
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Patent No. 6399373
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LOCATION: 72794
OTHER INFORMATION: 5-124-273
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APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CL001164DIV
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
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  CTCAGGAGTAGAGGTGATCTCTGCTCGAAAGAGAAAATAGAATGAAAATATTCTCCGGGCC
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Patent No. 6680188
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NAME/KEY: misc_feature
LOCATION: (1)...(174493)
OTHER INFORMATION: n = A,T,C or
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OTHER INFORMATION: 5-145-24
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                                                  LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A or FEATURE:
NAME/KEY: allele
LOCATION: 93714
OTHER INFORMATION: 5-128-60 : polymorphic base deletion
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LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A
FEATURE:
LOCATION: 150329
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OTHER INFORMATION: 5-140-120 : polymorphic base
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OCATION: 108149
YHER INFORMATION: 5-135-198 :
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OTHER INFORMATION: 99-1442-224
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THER INFORMATION: 5-130-276
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OCATION: 106940
THER INFORMATION: 5-133-375
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OCATION: 108106
THER INFORMATION: 5-135-155
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LOCATION: 134374
DIHER INFORMATION: 5-140-361
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OCCATION: 108471
THER INFORMATION: 5-136-174
FRATURE:
LOCATION: 88073
OTHER INFORMATION: 5-127-261
FEATURE:
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LOCATION: 99098
DIHER INFORMATION: 5-130-257
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OCATION: 108308
WHER INFORMATION: 5-135-357
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THER INFORMATION: 5-129-144
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NAME/KEX: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84
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OCATION: 103806
THER INFORMATION:
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LOCATION: 134362
OTHER INFORMATION:
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NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
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OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
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JTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
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LOCATION: 97130...97177
LOCATION: 97130...97177
LOCATION: POLYMOTPHIC fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 99075...99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
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LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
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NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
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NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
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LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
                                                                                                  LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
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OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
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OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
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NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
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OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
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LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic
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NAME/KEY: allele
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10200 CCCCAAGTGCTGGGATTACAGACATGAGCCACTGCGCTGGGCCCCATGCGCCTCCATTT 10259
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                               1992 TAGCTAAGTGTGGTGGCGCATGCCTGTAATCCCAGCTACTTGGGAGGGTGAGGCAGGAGA
                                                                                                                                            Sequence 3, Application US/09735934A
Patent No. 6372468
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND TITLE OF INVENTION NUMBER: US/09/735,934A
CURRENT APPLICATION NUMBER: 2000-12-14
NUMBER OF SEC ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                      86253 TAGCCAGGCATGGTGCGTGCTGTAATCCCAGCTACTCTGGAGGCTGAGGCAGGAG
                                                                                                                   2052 ATTICITGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGATCACACCACTGCACTCCAG
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Pred. No. 4.8e-66;
0; Mismatches 233; Indels 31;
FEATURE:
NAME/KEX: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
                                                                                                                                                                                                                                                                                                                                                                                                                       IDS9
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                                                                                 FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375
                                                                                                                                                                       FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375
                                                                                                                                                                                                                                                             FEATURE:

LOCATION: 108084..108130

OTHER INFORMATION: polymorphic fragment 5-135-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198
FEATURE:
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LOCATION: 108127..108177
CTHER INFORMATION: polymorphic fragment 5-135-198
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCARION: 108084..108130
OTHER INFORMATION: polymorphic
FEATURE:
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Best Local Similarity 66.7%;
Matches 529; Conservative
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10677 Arccas 10682
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ORGANISM: Homo sapiens
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US-09-851-896-3/c
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Best Local Simi]
Matches 504; (
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US-09-851-896-3
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APPLICANT: LI, Jiayin et al

TITLE OF INVENTION: SOCIATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND ITILE OF INVENTION: THERROW

FILE REFERENCE: CLOOOSSIDIV

CURRENT PAPLICATION NUMBER: US/10/060,332

CURRENT FILING DATE: 2002-02-01

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                   10498 TAGAAA-AATTAGCTGGTGTGGTGGCGGGTACCTATAATCCCAGCTACTCGGGAGGCTG
                                                                                                                  AGGCAGGAGAATTTCTTGAACCCG-GGAGGCAGAGGTTGCAGTGAAGCGAGATCACACA
                                                                                                                                                                       10142 --AGACGGGGTTTCACCATGTTGGCCAGGCTGGTTTCAAGTAATCCACCCTCCTCAGCCT
 TGAGGTCAGGAGTTCAAAACCAGCCTGGCCAACATGGTGAAAACCCCGTCTCTACTAAAAA
                                                                                                                                             10557 AGGCAGGAGAATCATTTGAACCTGAGGGTGGAGGTTGCAGTGAGCCGAGATCATACCA
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7.8%; Score 307.6; DB 4; Length
Best Local Similarity 67.6%; Pred. No. 3.4e-66;
Matches 491; Conservative 0; Mismatches 229; Indels
                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10060332 Patent No. 6528294
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ORGANISM: Homo sapiens
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LENGTH: 43950
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US-10-060-332-3
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Sequent No. 6410325
SERRAL INFORMATION:
SECURIAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: APACHEW T. Watt
TITLE OF INVENTION: BATREENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPEND TITLE OF INVENTION: BATREESSION
FILE REFERENCE: RTS-0220
CURRENT FAPILICATION NUMBER: US/09/851,896
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                                      10617 Tridicacricia de carcades de caracadas de controlas de caracadas de 10676
                                                            10380 decacedradercacereranareceaecacririoscadeceaaeceaaeceaeaearea-- 10437
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GGCGTGGTGGCTCATGCCTGTAATCCCAGCACTT
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us-10-016-725-15_copy_1_3958.rni

32440 AATTITIGIATITITAGIGGAGAAGGGGTTTCACCAIGITIGGCCAGGCTGGTCTCGAACT 32381 1092 CCAGTGAATATTCAIGTATACATTTGIGGGGCATATGTTTCATTT 1138	32200 GCTGTGAGAAAGAGGGGAGATAGCATACTGTGTCTGCCTGTTTGTGCTGAACGAAACCC 31141 1304 TTGAGTGAGATACAACTCAACTCAACTGAGAATTAGGGAGTTAGGGGGT 1163 1314 CAGGAGGAGCAACCAG-AAGTGAACGAGACTGCTTACTACAGGGGGTAGGGGAGA 32083 1309 TAGAGTGAAATTGAATTATTATTATTATTATTATTATTAT
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US-09-735-934A-3/C
15-09-735-934A-3/C
5 Sequence 3. Application US/09735934A
5 Patent No. 6372468
6 GENERAL INFORMATION:
7 APPLICANT: LI, Jiayin et al
7 TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
7 TITLE OF INVENTION: THEREOF
7 TITLE OF INVENTION: THEREOF
7 TITLE OF INVENTION: THEREOF
7 TITLE OF INVENTION: THEREOF
7 TITLE OF INVENTION: THEREOF
7 TITLE OF INVENTION: THEREOF
7 TITLE OF INVENTION: THEREOF
8 TITLE REPERBRENCE: CL000821.
8 CURRENT APPLICATION NUMBER: 105/09/735,934A
8 CURRENT FILING DATE: 2000-12-14
8 NUMBER OF SEQ ID NOS: 4
8 SOFTWARE: PRESEQ for Windows Version 4.0
8 SEQ ID NO 3
8 LENGTH: 43950
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Best Local Similarity 68.2%; Pred. No. 4.8e-65;
Matches 492; Conservative 0; Mismatches 200; Indels 29; Gaps
                                    31309 AAAAAAAAAAAAAAAAAAAGGAACCAACTA 31278
2142 AAAAACAAAAACAAAAGAATTAAGCAAATTA 2173
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 10, April Sequence 24494, A Sequence 24494, A Sequence 14991 Sequence 1169, April Sequence 1569, April Sequence 1569, April Sequence 1569, April Sequence 156, April Sequence 7810, April Sequence 7810, April Sequence 7810, April Sequence 7810, April Sequence 7810, April Sequence 7810, April Sequence 7810, April Sequence 7810, April Sequence 7810, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Sequence 2278, April Seq
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1: /cgn2 6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
2: /cgn2 6/ptodata/1/pubpna/DST_NEW PUB.seq:*
3: /cgn2 6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
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10: /cgn2 6/ptodata/1/pubpna/USO9 PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-087-192-814

US-10-087-192-814

US-10-087-192-81

US-10-087-192-52

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0y 3481 GCTCCCGACGCGCACAGGCCCCACGGCGGGGGGGGGGGG	RESULT 2 US-10-087-192-10 Sequence 10, Application US/10087192 Publication No. US20020182586A1 GENERAL INFORMATION: APPLICANT: Morris, David W. APPLICANT: Morris, David W. TITLE OF INVENTION: CANCER TITLE OF INVENTION: CANCER TITLE OF INVENTION: CANCER CURRENT APPLICATION NUMBER: US/10/087,192 CURRENT FILING DATE: 2002-03-01 PRIOR FILING DATE: 2000-12-22 PRIOR PELING DATE: 2001-03-02 PRIOR FILING DATE: 2001-03-02 NUMBER OF SEQ ID NOS: 2059 SOFTWARE: FastESE for Windows Version 4.0 LENGTH: 37698 LENGTH: 37698 LENGTH: 37698 US-10-087-192-10	Query Match 99.3%; Score 3929.8; DB 13; Length 37698; Best Local Similarity 99.3%; Pred. No. 0; Matches 3953; Conservative 0; Mismatches Qy 3 GAATTCATCCATTTAAATCAATTTAATGCTTTTAGTAATTCACAGGTTGTGCAT C) 6280 GAATTCATCCATTTAAATCAAATTTAATGCTTTTAGTAATTCACAGGTTGTGCAT Qy 63 CCATCACAAATCCATTTTAAATCATTTAATACTCCCAAAAATAAAACCTGCATTCCTTAG Db 6340 CCATCACACATTTTAGAACAGTTTTAATACTCCCAAAAATAAAACCTGCATTCCTTAG Db 6340 CCATCACCCCCCAACATCTCCATTTAATACTCCCAAAAATAAAACCTGCATTCCTTAG CA 123 CCATCACCCCCCAACATCTCCATCTCCTACCAAAAATAAAAACCCTGCATTCCTTAG CA 123 CCATCACCCCCCAACATCTCCATCCTTCCAAGCCTTGGGCAACCACCAATCTTAT CA 123 CCATCACCCCCCAACAACCTCCCATCCTTCCAAGCCTTGGGCAACCCCAAATCTATT CA 123 CCATCACCCCCCAACAACCTCCCTTCCCAACCCTGGGCAACCACCAAATCTACTT CA 123 CCATCACCCCCCCAACAACCCTCCCTTCCCAACCCTGGGCAACCCCAAATCTATT
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Qy 3482 CTCCCGACGCGGCATGCCGGCCCACGCGGCGGCGGCGGAAGAAGCTGAGAAGCH Db 9759 CTCCCGACGCGGATGCCGGCACAGGCCCGGCGGAGAAAGCTGAGAAGCTGAAAGCGCGAAGAGAAGCTGAAAGCTGAAAGCTGAAAGCTGAAAGCTGAAAGCTGAAAGCTGAAAGCTGAAGAAGCTGAAAGCTGAAAGCTGAAACACGCGAATGCCCCCAAGAACACGCCGAATGCCCCCAAGAACACGCCGAATGCCCCCAAGAACACGCCGAATGCCCCCAAGAACACGCCCAATGACGAATTGCCCCAATGACGAATTGCCCCCAATGACGACCCCAAGAATTGCCCCCAATGACGACCCCAAGAATTGCCCCCAATGACGACCCCAAGAATTGCCCCCAATGACGACCCCAAGAATTGCCCCCAATGACGACCCCAAGAATTGCCCCCAATGACGACCCCAAGAATTGCCCCCAATGACGACCCCAAGAATTACCCCTTCCGCCCAATGACGCCCAAGAATTACCCTTCCGCCCAATGACGCCCAAGAATTACCCTTCCGCCCAATGACGCCCCAAGAATTACCCCTTCCGCCCAATGACGCCCCAAGAATTACCCCTTCCGCCCAATGACGCCCCAAGAATTACCCCTTCCGCCCAATGACGCCCCAAGAATTACCCTTCCGCCCAATGACACCCCCAAGAACCCCCCAAGAATTACCCTTCCAAGAACCCTTCCAATGACAACCCTCCAATGACACCCCCCAAGAACCCCCCAAGAACCCCCCAAGAACCCCCC	USA10-027-032-24494/c Sequence 24494, Application US/10027632 Sequence 24494, Application US/10027632 Sequence 24494, Application No. US20020198371A1 Sequence 24494, Application No. US20020198371A1 Sequence 24494, Application No. US20020198371A1 SEMERAL INFORMATION: Identification and Mapping of Single Nucleotide TITLE PORTENTION: Identification in the Human Genome TITLE PORTENTION: Identification North Nor
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Publication No. US20030204075A9

Fublication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE OF INVENTION: DATE: 10827.129

CURRENT FILING DATE: 2002-04-30

FRICR FILING DATE: 2000-07-12

FRICR APPLICATION NUMBER: US 60/218,006

FRICR FILING DATE: 2000-04-20

FRICR FILING DATE: 2000-04-20

FRICR FILING DATE: 2000-04-20

FRICR FILING DATE: 2000-04-20

FRICR FILING DATE: 2000-04-20

FRICR FILING DATE: 2000-03-29

FRICR FILING DATE: 1999-11-23

FRICR FILING DATE: 1999-11-23

FRICR FILING DATE: 1999-09-28

FRICR FILING DATE: 1999-09-28

FRICR FILING DATE: 1999-09-28

FRICR FILING DATE: 1999-09-28

FRICR FILING DATE: 1999-09-08

FRICR FILING DATE: 1999-09-08

FRICR FILING DATE: 1999-09-08

FRICR FILING DATE: 1999-09-08

FRICR FILING DATE: 1999-09-08

FRICR FILING DATE: 1999-09-08

FRICR FILING DATE: 1999-09-08

FRICR FILING DATE: 1999-09-08

FRICR FILING DATE: 1999-08-09

FRICR FILING DATE: 1999-08-09

SECTIORER: FREESEQ FOR Windows Version 4.0

SECTIORER: FREESEQ FOR WINDOWS TIPPE: DNA
                                                                                                                        .088 TACTCCAGTGAATATTCATGTATACATTTGTGGGGCATATGTTTTCATTTCTGTTGGGT
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APPLICANT: Hayden, Michael R.
APPLICANT: Brownlie, Alison J.
APPLICANT: Brownlie, Alison J.
APPLICANT: Brownlie, Alison J.
APPLICANT: Miyazaki, Makoto
APPLICANT: Miyazaki, Makoto
APPLICANT: Gray-Reller, Mark P.
APPLICANT: Artie, Alan D.
TITLE OF INVENTION: Methods and Compositions Using Stearcyl-CoA Desaturase
TITLE OF INVENTION: to Identify Triglyceride Reducing Therapeutic Agents
FILE REFERENCE: 760050-7
CURRENT APPLICATION NUMBER: U.S. 60/184,526
FRIOR APPLICATION NUMBER: U.S. 60/184,526
FRIOR APPLICATION NUMBER: U.S. 60/221,697
FRIOR APPLICATION NUMBER: U.S. 60/221,697
FRIOR APPLICATION NUMBER: U.S. 60/255,771
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         Score 630.6; DB 16; Length 631;
Pred. No. 1.7e-158;
1; Mismatches 0; Indels 0;
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         15.9%;
99.8%;
Query Match
Best Local Similarity 99.8<sup>3</sup>
Matches 630; Conservative
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Query Match
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                                                                                                                   Length 617;
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OCANCER
TITLE OF INVENTION: OCANCER
FILE REFERENCE: 529452000122
CURRENT FILING DATE: 2002-03-01
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 814
LENGTH: 59725
                                                                                                               Score 498.4; DB 10;
Pred. No. 5.7e-123;
0; Mismatches 1;
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Publication No. US20020182586Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGACCTCCACGCACCGCGG 3958
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                                                                                                                  12.6%;
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ 1D NOS: 6
SOFFWARE: Patentin Ver. 2.1
SEQ 1D NO 1
                                                                                                               Query Match
Best Local Similarity 99.8
Matches 499; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                             TYPE: DNA ORGANISM: Homo sapiens
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US-10-087-192-814/c
                                                                              ; ORGANISM: Hor
US-09-792-468B-1
                                                   LENGTH: 617
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APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: UP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
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; LOCATION: (9233)...[9332)
; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-1569
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Sequence 1569, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA

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10703 TTTAGCTATTCTTAŤTŤTCAŤTCTTAŤTTTCCATTAŤGGATCTACAČÁČŤGAĞTTTATTA 10644
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                             1936 CAAAACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGC
                                                                   1806 -GAGACCATTCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAATAC-AAAATTAGC
                                                                                                                                                       1864 CGGGAGTGGTGGTGCCTTTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAATGG
                                                                                                            1996 TAAGIGIGGGGCAIGCCIGIAAICCCAGCIACTIGGGAGGGIGAGGCAGGAGITI
                                                                                                                                                                                                    2056 CITGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGATCACACCACTGCACTCCAGCCTG
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Pred. No. 8.3e-85;
0; Mismatches 221; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morais, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: ANGRER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR PELICATION NUMBER: US/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FRELENG FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                     ; LOCATION: (1)...(23618)
; OTHER INFORMATION: n = A,T,C or US-10-087-192-4
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Best Local Similarity 69.3%;
Matches 503; Conservative
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ORGANISM: Homo sapiens
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US-10-087-192-4/c
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                                                                                                                         GGCTGTATTTTTATTGTTGAGACAAGGTCTCACTATGTTGCCATGATCCCCCCACCTCCA 1004
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693 CTCAAGTGATCCTCCTGCCTCAGCCTGCCTAATAGCTAGGAGCACAGGTGTGTGCCACAA
                                          753 TGCCTAGCTAATTTTTAAATT----TTTTTTTGTAGAGATGGGATCTCACTATGTTGCCTA
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APPLICANT: Engelhard, Eric K.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO S: 2059
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Pred. No. 1.5e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-087-192-52

Sequence 52, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
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Best Local Similarity 55.0%;
Matches 1044; Conservative
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ORGANISM: Homo sapiens
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FEATURE: NAME/KEY: CDS LOCATION: (5639)(5722) FEATURE: NAME/KEY: CDS LOCATION: (5864)(5974) FEATURE: NAME/KEY: CDS LOCATION: (7902)(8032) FEATURE: NAME/KEY: CDS LOCATION: (8121)(8227) FEATURE: NAME/KEY: CDS LOCATION: (9197)(9294) FEATURE: NAME/KEY: CDS LOCATION: (9375)(9470) FEATURE: NAME/KEY: CDS LOCATION: (9898)(10084) FEATURE: NAME/KEY: CDS LOCATION: (10431)(10523) LOCATION: (10431)(10523) LOCATION: (11713)(11786) LOCATION: (11713)(11786)	Query Match 8.8%; Score 349.8; DB 16; Length 12394; Best Local Similarity 55.2%; Pred. No. 3.8e-82; Matches 1016; Conservative 0; Mismatches 742; Indels 81; Gaps 14; Qy 370 TATTATTAGAGACAGGTTCTCACTCTGTCACCCCAGGCTGCAGTGCACACACA	QY 430 GCTCACTGTAACCTCAAACTCCTGGGCTCAAGTGATCCTACCTCCAGCCTCCAGGGTA 489 Db 3664 GCCGGCTACAACCTCTGCCTCCCAGGTTCTTGTGCCTCAACCACCTGAGTA 3723 QY 490 GCTAGGACTACAGGCACACAGCCATACCTGGCTAATTTTTTTT	ON 550 AIGTATTCATTTCTTTTTGTTGTTTGTTTGAATAGGGTCTCACTTTGTTA 609 Db 3782 GTAGAGACAGGGTTTTGCATTTGTTGTTTTGAACTCCTGACCTCAACTAAT 3841 Qy 610 CCCAGGCTGGAGGCAGTGGTGACAGCTGACTCCTGACCTCCAGGATAT 3841 Db 3842 CGCCCCACCTCGAACTGCTGATTTACAGGCTTGAGCCAGCAT 3894 Qy 670 TGATCCTCCTGCTCACCTCCCAAGTAGCTGGTATTACAGGCTGAGCCAGCAT 3894 Qy 729 GGCTGATTTTTTTTTTTTAAACACAGAAACTGGATTTAGATCTGAAACTTGAAACTGGAATTTTTTTT
1571 TGGGACTACAGGCACTTCCCACCAGGCTGATTTTTGTATTTTTAGTACAGGTGGG 1630 1637 TGGGACTACAGGCACCAGGCCATTTTTTGTATTTTTAGTACAGACAG	Qy 1960 GAAACCCCGTCTCTACTAAAATACAAAAATTAGCTAAGTGTGGCGCATGCCTGTA 2019 Db 6007 GAAACCCCGTGTCTACTAAAATAC-AAAATTAGCCAGGCATGGTGGCCTGTA 6065 Qy 2020 ATCCCAGCTACTTGGGGGGGGGGGGGGGGGGGGGGGGGG	QY 2080 CAGTGAAGCGACACCACTGCACTCCAGCCTGGGGAGAGAGA	RESULT 11 US-10-181-875-10 Sequence 10, Application US/10181875 Publication No. USZ0030216333A1 SEQUENCEAL INFORMATION: APPLICANT: Brett P. Monia APPLICANT: Madeline M. Butler APPLICANT: Madeline M. Butler APPLICANT: Madeline M. Butler APPLICANT: Madeline M. Butler APPLICANT: Madeline M. Butler APPLICANT: Madeline M. Butler APPLICANT: Madeline M. Butler APPLICANT: Madeline M. Butler APPLICANT: Madeline M. Butler APPLICANT: Madeline M. Butler APPLICANT: Madeline M. Butler APPLICANT: Madeline M. Butler APPLICANT: Madeline M. Butler APPLICANT: MADELINE MATE: 2002-01-21 FILE REFERENCE: 12304 CURRENT FILING DATE: 2000-01-21 NUMBER OF SEQ ID NOS: 88 CURRENT: 12394 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS LOCATION: (115)(397) FEATURE: NAME/KEY: CDS LOCATION: (2438)(2625)

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1981 ATACAAAAATTAGCTAAGTGTGGTGGCGCATGCCTGTAATCCCAGCTACTTGGGAGGGT
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8.7%; Score 342.8; DB 9;
Best Local Similarity 57.5%; Pred. No. 4.9e-80;
Matches 848; Conservative 0; Mismatches 552;
                                                                                                                                                                                                 2161 ATTAAGCAAATTAGACA 2177
                                                                                                                                                                                                                               4332 ACAAACAAACAAACA 4348
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ORGANISM: Homo sapiens
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US-09-880-107-2278
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                                                 1214 GAGGCAGGAGAATCACTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCAAGATCACACCA
                                                                                       GAGGCAGGAATTTCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGATCACACCA
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                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
FILOR application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Retentin Ver. 2.0
SEQ ID NO 7809
LENGTH: 29163
                                                                                                                                                                                                                                                       Sequence 7809, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
                                                                                                                                                2161 ATTAAGCAAATTAGACA 2177
                                                                                                                                                                              4334 ACAAAACAAACAAACA 4350
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US-09-764-891-7809
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515; Conserv
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US-09-764-891-7809
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Matches 515
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2041 GAGGCAGGAGAATTTCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGATCACACCA
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Fatent No. US20020142981A1
Fatent No. US20020142981A1
FAPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 4421-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
FRIOR FILING DATE: 2000-06-14
FRIOR FILING DATE: 2000-06-14
FRIOR FILING DATE: 2000-06-14
FRIOR FILING DATE: 2000-06-16
SOFTMARE PATENTION NUMBER: US 60/237,054
FRIOR FILING DATE: 2000-10-02
SOFTMARE PATENTION NUMBER: US 60/237,054
FRIOR FILING DATE: 2000-10-02
SOFTMARE PATENTION NUMBER: US 60/237,054
FRIOR FILING DATE: 2000-10-02
SOFTMARE PATENTION VOY: 2.1
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US-09-880-107-2278
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US-10-235-192A-34

Sequence 34, Application US/10235192A

Sequence 34, Application US/10235192A

Sequence 34, Application US/004389A1

GENERAL INFORMATION:

APPLICANT: McCarthy, Jeanette

TITLE OF INVENTION: Methods and Compositions for Identifying

TITLE OF INVENTION: Risk Factors for Abnormal Lipid Levels and the Diseases

TITLE OF INVENTION: and Disorders Associated Therewith

FILE REFERENCE: MMI-011

CURRENT APPLICATION NUMBER: US/10/235,192A

CURRENT APPLICATION NUMBER: 2002-09-04

NUMBER OF SEQ ID NOS: 49

SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Miklos I Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://imag-llnl.gov
Plate: LiAMI1746 row: C column: 18
High quality sequence stop: 576.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 579)
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BI559696 579 bp mRNA linear EST 05-SEP-2
603252566F1 NIH_MGC_97 Homo Bapiens cDNA clone IMAGE:5294921 5',
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                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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/clone_lib="NNH MGC 119"

/note="Organ: brain, Vector: pCMV-SPORT6; Site 1: Not1;

Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Assage insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for
NTAAATCATACAATTTAATGGCTNTTAGTATATTCACAGGTTGTGCATCCATCA 60
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Library Preparation: Life Technologies, Inc.

Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

Sequencing by: Incyte Genomics, Inc.

Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

Sequencing by: Consortium/LIML at:

[through the I.M.A.G.E. Consortium/LIML at:

[through the I.M.A.G.E. Consortium/LIML at:

LibMl1416 row: n column: 16

quality sequence stop: 741.

Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5167695"
/tissue_type="medulla"
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(Invitrogen). Research Genetics tracking code 013. Note: this is a NHH_MGC Library."
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Homo sapiens RAD1 homolog (S. pombe), mRNA (cDNA clone IMAGE:5582524), with apparent retained intron.
                                                                                                                                                                                                          Length 754;
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Pred. No. 1.1e-41;
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Homo sapiens
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VIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapba-refmail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc mgc@nhgri.nih.gov
Contact: nisc mgc@nhgri.nih.gov
Contact: N. Bouffeard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Blakesley, R. W., Bouffeard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hagnishi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J. W.
TBurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINN at: http://image.llnl.gov Series: IRAK Plate: 79 Row: d Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein This clone has the following problem: retained intron.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                835
Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITCACCCIGGCIGGAGGCAGIGGIGIGAICTCAGCICACTGCAACTITCGCCICCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1116 rercaccededresadresadresadresadresecretadresadesecretades
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         894 TTCCCAAAATGCTGGGATTACAGGTGTGAGCCACCACTCCCGGCCTAAAATAGTTTT
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mol type="mRNA"
db xref="taxon:9606"
/clone="INAGE:5582524"
/tissue type="Testis, embr
/clone lib="NIH MGC_92"
/lab_host="DH10B"
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CDNA Library Preparation: Number of Health Intramural CDNA Library Preparation: Number of Health Intramural CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing Dy: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web Site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov/
Bakkeley.R.W. Bouffard, G.G. Breen, K., Brinkley, C., Beroks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Madner, O.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1661 ACTITITGCIGICALAATIGITGIAACTATIGITCCITTITGCIGAGGIAGGCCCCCCAGA 1720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT-----CCCGACCTCTGCTGATCCGTATGCCTCGGCCTCCCAAAGTGCTGGGATT 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1721 CCAAAAAAAAATAAATCTTAGAATCCAAATCAGTGTGGTTTGACCACTGTCACTTGAG 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACCACAGTGTGACCAGGGCCTCAGGAGTAGAGGTGATCTCTGCTCGAAAGAGAAATAGA 1840
                                                                                                                                                                                                                                                                                                                                                                                                                                       through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Series: IRAL Plate: 39 Row: p Column: 13
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAATTCTCCTGCTTCAGCCTCCCAAGTAGCTGGGACTACAGGCACTTCCCACCATGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1421 AAAATAATAAAAAATCACAATTTTTTTTTTTTTTTGAGAAAGAGTCTTGCTTTTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGCTGGAGGGCAGTGGTGTGTCTCAGCTCACTGCAACTTTCGCCTCCCGGGTTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1032 ACATGCGTGAGCCACCGTGCCCGACAATAGATGTCTTTTAATTTTCTGGAGGAAAAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  741 ACAAACGIGAAAIAGAIGICTITITITITITITIGAGAIGGAGITITICACICTIGITACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.3%; Score 290.6; DB 11; Length 2076; 67.2%; Pred. No. 2.8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identity to protein
This clone has the following problem: retained intron.
Location/Qualifiers
               M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mknk"
/mol_type="mknk"
/db xref="taxon:9606"
/clone="IMAGE:5094058"
/tissue type="Lymph, Burkitt lymphoma"
/clone_lib="NIH MGC"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.8e-35;
); Mismatches 214;
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          Procurement: Louis M.
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AAAIGIACAAAAITCCAICCIIACIGAGCIGAITIAIAITIGITIIAAAITCITITIA 775
                                                                                                                                                                                                                                                                                                                                                                                594 CACCIGIAGICGIAGCIAITIGGGAAGCIGAGAIGGAGGAGGAIGCITIGAGCCIAGGAGAI 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534 TGAGGCTGGAGTGAACTGTAATCCTACAACTGTACTCCAGCCTGGGCAACAGAGCAAGAT 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2076)
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2076 bp mRNA linear HTC 19-NOV-20 HOMO sapiens sialophorin (gpL115, leukosialin, CD43), mRNA (cDNA clone IMAGE:5094058), with apparent retained intron.
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Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                           GATTCAACTITTAAAAAATACATTAGGCCAGGCATGATAGCTCACGCCTGTAATCCCAGC
                                                                                                                                                                                                                                        AACATGGTGAAACCCCGTCTCTACTAAAATACAAAAATTAGCTAAGTGTGGTGGCGCA
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                                                                                                                                                                                     714 ccriridesagecceaescesafesarrecricascricaseacricasearrasccraese
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. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      474 CITGICCAAAAIAAAAAAAAAAAAAAAAAACTGAGAICAAAAIAAAIITAG 426
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
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KEYWORDS
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2772)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 73 Row: i Column: 4
This clone has the following problem: retained intron.
Location/Qualifiers
1. .2772
1198 AGGCCGAGGCAGGTGACTGAGGTCAGGAGTTCAAGACCAGCCTGACCAACATGGT
                                                                                                                             2020 ATCCCAGCTACTTGGGAGGGTGAGGAGAGAATTTCTTGAACCCGGGAGGCAGAGGTTG
                                                                                                                                                               1313 Arcccadcraciridedadecreadedadadarcccrreaacccadeaegree
                                                                                          1258 GAAACCCTGTTTC----AAATACAAAATTAGCTGGGGGGTGGTGGCGGGGCACCTGTG
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael W.D., Ph.D.
Tissue Procurement: Michael W.B., Ph.D.
CONA Library Preparation: Michael J. Brownstein (NHGRI) & Sh
Toshiyuki and Piero Carninci (RIKEN)
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Brin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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/db_xref="taxon:9606"
/clone="IMAGE:5263792"
/tissue_type="sain, hippocampus"
/clone_lib="NIH_MGC_95"
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lab host="DH10B"
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BC038630.1 GI:24116283
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Best Local S
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1441 TTTTTTTTTTTTTTTGAGAAAGAGTCTTGCTCTT-TCACCCTGGCTGGGCAGTGGT 1499

Conservative

Similarity

Best Local Sim Matches 508;

DB 11; Length 2772;

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1919
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TITITITITITIGETAAGACGGAGTTITIGCTCTTGTCTCCCAGGCTGGAGTGCAATGGT 2694
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Wataryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2772)
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Direct Submission
Submitted (15-02-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                              GCCATCTCGGCTGGCTGCAAACTGCACCTCCCGGGTTCAACAGATTCTCCTGCCTCAGCC
                                                                                                                                                                                                                                                         2633 TCCCAAGTAGCCGGAACACACACACGCCCACGCCCAGGCCAATTTCTGTATATTTA
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                                                                                        GIGATCTCAGCTCACTGCCAACTTTCGCCTCCCGGGTTCAAGCAATTCTCCTGCTTCAGCC
                                                                                                                                                                                                                TCCCAAGTAGCTGGGACTACAGGCACTTCCCCACCATGCCCAGCTGATTTTTGTATTTTTA
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Contact: MGC help desk
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BC035510.1 GI:23271054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1621 TAGAGATGGGATTTCACTTTGTTGGCCAAGCTGGTCTCAAACTTTTTGCTGTCTCATAATTG 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2250 TAGAGGCAAGGTTCACCATGTTGGTCAGCTGGTTGAACTCCTGACCTCAGGTGACCT 2309
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                                                      Shiraki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                           contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anura
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CINA Library Preparation: Michael J. Brownstein (NHGRI) &
Toshiyuki and Piero Carninci (IKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.2%; Score 283.4; DB 11; Length 2772; Best Local Similarity 66.1%; Pred. No. 3e-34; Matches 486; Conservative 0; Mismatches 216; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2423 ACAAGCAAGATAGTTGATATCAAGAA-------
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/mol_type="manka,"
/mol_type="manka,"
/db.xref="taxon:9606"
/clone="INAGE:553792"
/tlssue_type="Brain, hippocampus"
/clone="line="NIH_MGC_95"
/lab_hoft="PH10B"
/note="Vector: pBluescript"
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1 (bases 1 to 749)
NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: ATCC
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DNA Sequencing by: Agencourt Blossience Corporation
Clone distribution: MG clone distribution information can
found through the I.M.A.G.E. Consortium/Link at:
http://image.lln.gov
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Location/Qualifiers
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  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAL Plate: 39 Row: p Column: 13 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein This clone has the following problem: retained intron. Location/Qualifiers
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67.4%; Pred. No. 1.2e-32;
tive 0; Mismatches 206; Indels 30; Gaps
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231

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Gaps

24;

Length 749;

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DB 12;
          Score 269.4;
                                                                   0; Mismatches
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   Query Match
Best Local Similarity 97.8
Matches 273; Conservative
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AGENCOURT 6494267 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5729369
5', mRNA sequence.
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/note="Organ: brain; Vector: pCWV-SPORT6; Site_1: ECORV
/note="Organ: brain; Vector: pCWV-SPORT6; Site_1: ECORV
/note="Organ: brain; Vector: pCWV-SPORT6; Site_1: ECORV
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: ECORV
/note-1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCM
                                                            1803 CAGGAGTAGAGGTGATCTCTGCTCGAAAGAGAAATAGAATGAAATATTCTCCGGGCCAG 1862
                                                                                                                                                                                         1863 GCGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCATGTGGATCACCT 1922
                                                                                                                                                                                                                                                                                                                      1923 GAGGICAGGAGTICAAAACCAGCCIGGCCAACAIGGIGAAACCCCGICTCIACIAAAAI 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1983 ACAAAAATTAGCTAAGTGTGGTGGCGCATGCCTGTAATCCCAGCTACTTGGGAGGGTGA 2042
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                                                                                                               390 ATTIGCIGITAIGIATIACACAFAITATGAAGCAIATIAGAAIGIATITTCIGGGCCGG 449
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333 IGCAGAIGTGAGCCTCTGCACCCAGCCTATCCCTTTTTA---AGAIGGGAAAAATGGAA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            628 GTTGGGAĞGATTGCİTĞAGTCCAĞĞAĞTTTĞAĞĞGTATAATĞAACTATĞGGTGCAÇAĞCT 687
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1172)

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Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12726 row: i column: 18
High quality sequence stop: 618.

Location/Qualifiers
I. 1172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/tissue_type="hippocampus"
/lab_host="DH108"
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/mol_type="mRNA"
/db xref="taxon:9606"
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Riausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheder, C.F., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Garninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Boask, S.A., McZwan, P.J.,
McKernan, K.J., Mallek, J.A., Qunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Malk, M.M. Sodergren, E.J., Lu, X., Gabbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodriques, S.,
Bauchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
M.D. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (31-701-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 GGCAGCGGATAAAGGGGGCTGAGGAAATACCGGACACGGTCACCCGTTGCCAGCTCTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3800 GCCCTTACCTCCACGCGGGACCGCCCGCGCCAGTCAACTCCTCGCACTTTGCCCCCTGCTT
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Length 1172;
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HOMO Sapiens RAD1 homolog (S. pombe), mRNA (cDNA clone IMAGE:5582524), with apparent retained intron.
BC035771
                                                                         Indels
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Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
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ALS80585 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-JUN-2003
Homo sapiens cDNA clone CS0DJ015YK20 3-PRIME, mRNA sequence.
ALS80585.2 GI:31318853
                                                                                                                                                                                        1501 TGATCTCAGCTCAACTTTCGCCTCCCGGGTTCAAGCAATTCTCCTGCTTCAGCCT 1560
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Li, Massa I to 929
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12946748.
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRail: sequef@genoscope.cns.fr, www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8901.f For
Invitrogen. This sequence belongs to sequence cluster 8901.f For
thetp://www.genoscope.ns.fr/
cgi-bin/cluster.cgi?seq=CSODJ015BF10NP1&cluster=8901.f. Contact :
feng Librang Email : fliang@llfetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODJ015BF10NP1,
                                    1979 AAATACAAAAATTAGCTAAGTGTGGGGGCATGCCTGTAATCCCAAGGTACTTGGGAGG
                                                                                                                                        2039 GTGAGGCAGGAGAATTTCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGCGAGATCACAC
                                                                                      973 AAATACAAAATTAGCTGGGTGTGGTGGTGGTGTCTGTAATCCCAGCTACTTGAGAG
                                                                                                                                                                                                                                       1441 TITITITITITITITAGAAAAGAGICITGCTCTTTCACCCTGGCTGGAGGGCAGTGGTG
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62.2%; Pred. No. 2.8e-30;
live 14; Mismatches 245; Indels
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Matches
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AUTHORS
TITLE
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KEYWORDS
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                                                                 Galthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc mgc@nhgri.nih.gov
Contact: nisc mgc@nhgri.nih.gov
Athter,N., Ayele,K., Becketron-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouifard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins, E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,C.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                           found
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                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be for
through the I.M.A.G.E. Consortium/ILML at: http://image.llnl.gov
Series: IRAK Plate: 79 Row: d Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1501 TGAICTCAGCTCACTGCAACTTTCGCCTCCCGGGTTCAAGCAATTCTCCTGCTTCAGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511 GGATTAÇAĞTTCACTCCAGCCTCAATCTCCTAĞGCTCAAĞCAATCCTCCCATCTCAĞĞCTT
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.8%; Score 269.4; DB 11; Length 1910;
64.8%; Pred. No. 5.3e-32;
ive 0; Mismatches 236; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identity to protein
This clone has the following problem: retained intron.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 embryonal carcinoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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/clone="InAGE:5582524"
/tissue_type="Textis, emb./clone_lib="NIH MGC 92"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism≈"Homo sapiens"
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/ul.xt=1="ul-H-DF0-book"
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/dev stage="bddit"
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DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@ulowa.edu The following repetitive elements were found in this cDNA sequence: 9-305, >ALU (matched compliment) 326-387, >LIMB7#LINE/LI (matched compliment) 326-387, >LIMB7#LINE/LI Seq primer: MI3 FORWARD POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGITGIAACTAITGITCCITITGCTGAGGTAGGGCCCCCAGACCCAAAAAAAATAAATCT 1737
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                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mkNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                 location/Qualifiers
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Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          176 TGATYTCAGCTCGCTGCACCTCTGCCTCCCGTGTTCAAGCAATTYTCCTGCCTCAGCCT 235
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Contact: Robert Strausberg, Ph.D.
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